

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:20:05 ; Search time 20 Seconds

(without alignments)

1351.491 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MAMMEVQGSLSGTCVLV.....NEHLMDHEASFFGAFLVG 281

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	2.8	643	2 G75599	probable drug tran
2	8	2.8	950	2 T09076	hypothetical prote
3	7	2.5	51	2 S63590	insulin - duckbill
4	7	2.5	93	2 F84175	hypothetical prote
5	7	2.5	96	2 P80423	H4 protein - foxop
6	7	2.5	107	2 C90304	hypothetical prote
7	7	2.5	155	2 G72548	hypothetical prote
8	7	2.5	240	2 A39016	T-cell surface gly
9	7	2.5	247	2 D90053	hypothetical prote
10	7	2.5	251	2 T40807	hypothetical prote
11	7	2.5	263	2 T38003	hypothetical ser-t
12	7	2.5	327	2 H82736	hypothetical prote
13	7	2.5	329	2 D71887	ADFGlyceromanno-he
14	7	2.5	354	2 G71465	hypothetical prote
15	7	2.5	354	2 A81728	conserved hypothet
16	7	2.5	401	2 C82660	conserved hypothet
17	7	2.5	404	2 G90210	hypothetical prote
18	7	2.5	420	2 S53916	SUN4 protein precu
19	7	2.5	424	2 H84806	hypothetical prote
20	7	2.5	427	2 G71272	iron-sulfur cofact
21	7	2.5	428	2 E84192	zinc metalloprotei
22	7	2.5	429	2 B72109	GMP synthase CP059
23	7	2.5	429	2 C86512	GMP synthase limpo
24	7	2.5	442	2 AF2539	manganese transpor
25	7	2.5	475	2 T39359	probable udp-n-ace
26	7	2.5	511	2 T19496	hypothetical prote
27	7	2.5	554	2 A47503	epoxide hydrolase
28	7	2.5	565	2 C82280	sensor kinase cita
29	7	2.5	710	2 T22360	hypothetical prote

30	7	2.5	801	2 AE3032	conserved hypothet
31	7	2.5	801	2 G98253	hypothetical prote
32	7	2.5	809	2 T20430	hypothetical prote
33	7	2.5	913	2 D90183	ATP-dependent heli
34	7	2.5	926	2 T15683	hypothetical prote
35	7	2.5	979	2 JH0109	glycoprotein 14 pr
36	7	2.5	982	2 E88465	protein B0244.6 [1
37	7	2.5	1014	2 T36031	UDP-glucose-glycop
38	7	2.5	1377	2 T19214	excinuclease ABC c
39	7	2.5	1414	2 T33236	hypothetical prote
40	7	2.5	1847	2 E64477	replication factor
41	7	2.5	1891	2 T43262	calcium channel al
42	7	2.5	1975	2 B81192	hemagglutinin/hemo
43	7	2.5	1995	2 G81044	hypothetical prote
44	7	2.5	2015	2 B81989	hypothetical prote
45	7	2.5	3434	1 GNWVWV	genome polyprotein
46	6	2.1	47	2 T04365	ethylene responsiv
47	6	2.1	48	2 S78202	H+-transporting tw
48	6	2.1	55	2 AF2105	hypothetical prote
49	6	2.1	56	2 C60157	hypothetical prote
50	6	2.1	62	2 C97621	hypothetical prote
51	6	2.1	64	2 AG0025	probable bacteriof
52	6	2.1	65	2 AC0774	hypothetical prote
53	6	2.1	85	2 C91249	hypothetical prote
54	6	2.1	89	2 S78744	protein YDR363w-a
55	6	2.1	96	2 B82311	conserved hypothet
56	6	2.1	96	2 AE3205	transposase tnp [1
57	6	2.1	98	2 G91248	hypothetical prote
58	6	2.1	102	2 C95337	probable cytochrom
59	6	2.1	104	2 B98832	conserved hypothet
60	6	2.1	105	2 B86818	hypothetical prote
61	6	2.1	107	2 S09964	Ig kappa chain V-J
62	6	2.1	107	2 A44887	glucose transporte
63	6	2.1	109	2 F84012	hypothetical prote
64	6	2.1	112	2 AC2887	conserved hypothet
65	6	2.1	112	2 H97662	hypothetical prote
66	6	2.1	115	2 E25924	Ig kappa chain pre
67	6	2.1	116	2 C83166	probable chaperone
68	6	2.1	117	2 F97174	hypothetical prote
69	6	2.1	119	2 JQ2032	lambda 208 protein
70	6	2.1	122	2 D89803	conserved hypothet
71	6	2.1	128	2 AH0043	probable lipoprote
72	6	2.1	130	2 D64559	hypothetical prote
73	6	2.1	132	2 F66829	ribose ABC transpo
74	6	2.1	132	2 F70650	hypothetical prote
75	6	2.1	134	2 AC0855	probable regulator
76	6	2.1	135	2 B91078	transcription regu
77	6	2.1	135	2 T44999	hypothetical prote
78	6	2.1	137	2 S74888	hypothetical prote
79	6	2.1	137	2 D86944	conserved hypothet
80	6	2.1	137	2 T30095	hypothetical prote
81	6	2.1	137	2 F89954	conserved hypothet
82	6	2.1	143	1 WMBEGH	transcription regu
83	6	2.1	143	2 T43976	transactivator lim
84	6	2.1	143	2 B71372	conserved hypothet
85	6	2.1	145	2 AC0053	DNA-directed DNA p
86	6	2.1	146	2 C85923	probable regulator
87	6	2.1	149	2 H70581	hypothetical prote
88	6	2.1	151	2 A75297	hypothetical prote
89	6	2.1	152	2 B64485	hypothetical prote
90	6	2.1	152	2 T43088	traJ protein homol
91	6	2.1	154	2 F90546	deoxycytidylate de
92	6	2.1	157	2 A84402	hypothetical prote
93	6	2.1	161	2 H87183	integral membrane
94	6	2.1	162	2 T50253	Vacuolar ATP synth
95	6	2.1	165	2 S62563	adaptin complex sm
96	6	2.1	166	2 A75426	hypothetical prote
97	6	2.1	167	2 G95335	hypothetical prote
98	6	2.1	169	2 D72765	hypothetical prote
99	6	2.1	169	2 T31484	hypothetical prote
100	6	2.1	170	2 T48974	hypothetical prote

ALIGNMENTS

RESULT 1

G75599
 Probable drug transport protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: G75599
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: G75599
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-643 <WHI>
 A:Cross-references: GB:AE001862; GB:AE001825; NID:G6460468; PIDN:AAF12254.1; PID:G646054
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DRA0061
 A:Map position: 2

Query Match 2.8%; Score 8; DB 2; Length 643;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLIVITV 24

|||||

Db 231 VLIVITV 238

RESULT 2

T09076
 Hypothetical protein Cg1 (strain HB3) - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
 C:Accession: T09076
 R:Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellem, T.E.
 Cell 91, 593-603, 1997
 A:Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant
 A:Reference number: Z16556; MUID:98054002; PMID:9393853
 A:Accession: T09076
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-950 <SUX>
 A:Cross-references: EMBL:AF030690; NID:G2642510; PIDN:AAC47851.1; PID:G2642511
 C:Genetics:
 A:Gene: cgl

Query Match 2.8%; Score 8; DB 2; Length 950;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140

|||||

Db 361 SNTLSSPN 368

RESULT 3

S63590
 Insulin - duckbill platypus
 C:Species: Ornithorhynchus anatinus (duckbill platypus)
 C:Date: 19-Mar-1997 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: S63590
 R:Nourse, A.; Treacy, G.B.; Shaw, D.C.; Jeffrey, P.D.
 Biol. Chem. Hoppe-Seyler 377, 147-153, 1996
 A:Title: Platypus insulin: indications from the amino acid sequence of significant differ
 A:Reference number: S63590; MUID:97021710; PMID:8868070
 A:Accession: S63590
 A:Molecule type: protein

A:Residues: 1-30 <NOU2>
 A:Accession: S63590
 A:Molecule type: protein
 A:Residues: 31-51 <NOU1>
 C:Superfamily: insulin
 C:Keywords: hormone; pancreas
 F:1-30/1-51/Product: insulin #status experimental <MAT>
 F:1-30/Domain: insulin chain B #status experimental <BCH>
 F:31-51/Domain: insulin chain A #status experimental <ACH>
 F:7-37,19-50,36-41/Disulfide bonds: #status predicted

Query Match 2.5%; Score 7; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 EKGFIYI 184

|||||

Db 21 EKGFIYI 27

RESULT 4

F84175
 Hypothetical protein Vng0151c [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: F84175
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.
 Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: AB4160; MUID:20504483; PMID:11016950
 A:Accession: F84175
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-93 <STO>
 A:Cross-references: GB:AE004437; NID:gl0579798; PIDN:AAG18770.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: VNG0151C

Query Match 2.5%; Score 7; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 FVSVTNE 263

|||||

Db 13 FVSVTNE 19

RESULT 5

PS0423
 H4 protein - Toxoplasma gondii (fragment)
 N:Alternate names: diagnostic antigen H4
 C:Species: Toxoplasma gondii
 C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Sep-1997
 C:Accession: PS0423
 R:Johnson, A.M.; Illana, S.
 Gene 99, 127-132, 1991
 A:Title: Cloning of Toxoplasma gondii gene fragments encoding diagnostic antigens.
 A:Reference number: PS0423; MUID:91216437; PMID:2022319
 A:Accession: PS0423
 A:Molecule type: mRNA
 A:Residues: 1-96 <JOH>
 A:Cross-references: GB:M57302; NID:gl161914; PID:gl161915
 C:Genetics:
 A:Gene: H4

Query Match 2.5%; Score 7; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FQEEIKE 198

Db 2 FOEBIKE 8
|||||

RESULT 6

C90304
hypothetical protein SS01462 [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C/Accession: C90304
R/Sheng, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Accession: C90304
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-107 <KUR>
A/Cross-references: GB:AE006641; NID:gl3814690; PIDN:AAK41690.1; GSPDB:GN00155
C/Genetics:
A/Gene: SS01462

Query Match 2.5%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 FFGAFLV 280
|||||
Db 46 FFGAFLV 52

RESULT 7

G72548
hypothetical protein APE1675 - Aeropyrum pernix (strain K1)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C/Accession: G72548
R/Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah-
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: G72548
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-155 <KAW>
A/Cross-references: DDBJ:AP000062; NID:gs105244; PIDN:BAAS0676.1; PID:d1044462; PID:gs10
A/Experimental source: strain K1
C/Genetics:
A/Gene: APE1675

Query Match 2.5%; Score 7; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 TLSSPNS 141
|||||
Db 88 TLSSPNS 94

RESULT 8

A39016
T-cell surface glycoprotein CD7 precursor - human
N/Alternate names: T-cell leukemia antigen
C/Species: Homo sapiens (man)
C/Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 05-Nov-1999
C/Accession: A39016; S03520
R/Schanberg, L.E.; Fleenor, D.E.; Kurtzberg, J.; Haynes, B.F.; Kaufman, R.E.
Proc. Natl. Acad. Sci. U.S.A. 88, 603-607, 1991
A/Title: Isolation and characterization of the genomic human CD7 gene: structural simila
A/Reference number: A39016; MUID:91110576; PMID:1703303

A/Accession: A39016
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-240 <SCH>
A/Cross-references: GB:M37271; NID:gl80163; PIDN:AAA51953.1; PID:gi80164
R/Aruffo, A.; Seed, B.
EMBO J. 6, 3313-3316, 1987
A/Title: Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS cell ex
A/Reference number: S03520; MUID:88111517; PMID:3501369
A/Accession: S03520
A/Molecule type: mRNA
A/Residues: 1-240 <ARU>
A/Cross-references: EMBL:X06180; NID:g29819; PIDN:CAA29546.1; PID:g732757
C/Genetics:
A/Gene: GDB:CD7
A/Cross-references: GDB:119770; OMIM:186820
A/Map position: 17q25.2-17q25.3
A/Introns: 28/1
C/Keywords: glycoprotein; membrane protein; surface antigen; tandem repeat
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-240/Product: T-cell surface glycoprotein CD7 #status predicted <MAT>
F;145-180/Region: 9-residue repeats [X-P-P-X-A-S-A-L-P]

Query Match 2.5%; Score 7; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 NTLSSPN 140
|||||
Db 231 NTLSSPN 237

RESULT 9

D90053
hypothetical protein sarH2 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: D90053
R/Kuroda, M.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Og
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: D90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-247 <KUR>
A/Cross-references: GB:BA000018; PID:gl3702449; PIDN:BA843590.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A/Gene: sarH2

Query Match 2.5%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
|||||
Db 91 RIFVSVT 97

RESULT 10

T40807
hypothetical protein SPBP87.13 - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C/Accession: T40807
R/Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A/Reference number: Z21949
A/Accession: T40807
A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-251 <BEC>

A:Cross-references: ENBL:AL032684; PIDN:CAA21798.1; GSPDB:GN00067; SPDB:SPBP8B7.13

A:Experimental source: strain 972h-; clone pl p8B7

C:Genetics:

A:Gene: SPDB:SPBP8B7.13

A:Map position: 2

A:Introns: 54/1

C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBP8B7.13

Query Match 2.5%; Score 7; DB 2; Length 251;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DPNDDES 72

DB 73 DPNDDES 79

RESULT 11

T38003 hypothetical ser-thr rich protein - fission yeast (Schizosaccharomyces pombe) (fragment)

C:Species: Schizosaccharomyces pombe

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Nov-2000

C:Accession: T38003

R:Oliver, K.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the ENBL Data Library, June 1997

A:Reference number: Z21760

A:Accession: T38003

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-263 <OLI>

A:Cross-references: ENBL:Z97209; PIDN:CAB10128.1; GSPDB:GN00066; SPDB:SPAC19G12.16c

A:Experimental source: strain 972h-; cosmid c19G12

C:Genetics:

A:Gene: SPAC23A1.01c; SPDB:SPAC19G12.16c

A:Map position: 1

C:Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase

Query Match

Best Local Similarity 2.5%; Score 7; DB 2; Length 263;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 EETISTV 103

DB 177 EETISTV 183

RESULT 12

H82736

hypothetical protein XF0992 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: H82736

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: H82736

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-327 <SIM>

A:Cross-references: GB:AE003937; GB:AE003849; NID:g9105920; PIDN:AAF83802.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigh

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.J.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasal
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0992

Query Match 2.5%; Score 7; DB 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117

DB 164 SPLVRER 170

RESULT 13

D71887

ADPglyceromanno-heptose 6-epimerase (EC 5.1.1.3.20) gmhD homolog [similarity] - Helicobac

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000

C:Accession: D71887

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: D71887

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-329 <ARN>

A:Cross-references: GB:AE001509; GB:AE001439; NID:g4155350; PIDN:AAD06369.1; PID:g415535

A:Experimental source: strain J99

C:Genetics:

A:Gene: gmhD

C:Superfamily: ADPglyceromanno-heptose 6-epimerase; UDPglucose 4-epimerase homology

C:Keywords: isomerase

Query Match

Best Local Similarity 2.5%; Score 7; DB 2; Length 329;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RSNTLSS 138

DB 46 RSNTLSS 52

RESULT 14

G71465

hypothetical protein CT839 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C:Accession: G71465

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra

A:Reference number: A71570; MUID:9900809; PMID:9784136

A:Accession: G71465

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-354 <ARN>

A:Cross-references: GB:AE001356; GB:AE001273; NID:g3329299; PIDN:AAC68436.1; PID:g33293

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT839

Query Match

Best Local Similarity 2.5%; Score 7; DB 2; Length 354;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
|||||
Db 150 KENDRIF 156

RESULT 15

A81728
conserved hypothetical protein TC0227 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Accession: A81728
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: A81728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-354 <TET>
A;Cross-references: GB:AE002289; GB:AE002160; NID:g7190254; PIDN:AAF39099.1; PID:g7190254
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0227

Query Match 2.5%; Score 7; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
|||||
Db 150 KENDRIF 156

RESULT 16

C82660
conserved hypothetical protein XF1611 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: C82660
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: C82660
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-401 <SIM>
A;Cross-references: GB:AE003988; GB:AE003849; NID:g9106653; PIDN:AAF84420.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones,
M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1611
C;Superfamily: Escherichia coli hypothetical 48K protein (glnA-fdhE region)

Query Match 2.5%; Score 7; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 DAEGLY 240
|||||
Db 157 DAEGLY 163

RESULT 17

G90210
hypothetical protein purF-2 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: G90210
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Cha
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to Genbank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90210
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <KUR>
A;Cross-references: GB:AE006641; NID:gl3813800; PIDN:AAK40942.1; GSPDB:GN00155
C;Genetics:
A;Gene: purF-2

Query Match 2.5%; Score 7; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 YKSGIA 55
|||||
Db 35 YKSGIA 41

RESULT 18

S53916
SUN4 protein precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N2411; protein YNL066w; protein YNL1612
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Accession: S53916; S58712; S62994; S62998; S63945
R;Foehlmann, R.; Philippsen, P.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53896
A;Accession: S53916
A;Molecule type: DNA
A;Residues: 1-420 <POE>
A;Cross-references: EMBL:X86470; NID:g791101; PID:g791122
R;Bergez, P.; Doignon, F.; Crouzet, M.
Yeast 11, 967-974, 1995
A;Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XI
A;Reference number: S58711; MUID:96021608; PMID:8533472
A;Accession: S58712
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-420 <BER>
A;Cross-references: EMBL:U12141; NID:gl314216; PIDN:AAA99645.1; PID:g994821
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
R;Bergez, P.; Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62975
A;Accession: S62994
A;Molecule type: DNA
A;Residues: 1-420 <BEF>
A;Cross-references: EMBL:Z71342; NID:gl301944; PID:gl301945; MIPS:YNL066w
A;Experimental source: strain S288C
R;Foehlmann, R.; Philippsen, P.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62997
A;Accession: S62998
A;Molecule type: DNA
A;Residues: 1-420 <FOV>
A;Cross-references: EMBL:Z71342; NID:gl301944; PID:gl301945; MIPS:YNL066w

A;Experimental source: strain S288C
R;Poehlmann, R.; Philippse, P.
Yeast 12, 391-402, 1996

A;Title: Sequencing a cosmid clone of *Saccharomyces cerevisiae* chromosome XIV reveals 12
A;Accession: S63945
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-420 <POF>

A;Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60196.1; PID:g791122
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C;Genetics:

A;Gene: SGD:SUN4
A;Cross-references: SGD:S0005010; MIPS:YNL066W
A;Map position: 14L

A;Genome: nuclear

C;Superfamily: *Saccharomyces* NCA3 protein

C;Keywords: mitochondrion

F;1-46/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;46-420/Product: SUN4 protein #status predicted <MAT>

Query Match 2.5%; Score 7; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 VAVTVVY 37
|||||
DB 47 VAVTVVY 53

RESULT 19

H84806

hypothetical protein At2g38590 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C;Accession: H84806

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84806

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-424 <STO>

A;Cross-references: GB:AE002093; NID:g3786013; PIDN:AAC67359.1; GSPDB:GNO0139

C;Genetics:

A;Gene: At2g38590

A;Map position: 2

C;Superfamily: Arabidopsis thaliana hypothetical protein TIF15.9

Query Match 2.5%; Score 7; DB 2; Length 424;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 CFLKEDD 62
|||||
DB 122 CFLKEDD 128

RESULT 20

G71272

iron-sulfur cofactor synthesis protein nifS2 TP0863 [similarity] - syphilis spirochete

N;Contains: L-cysteine sulfotransferase (EC 2.8.1.-)

C;Species: *Treponema pallidum* subsp. pallidum (syphilis spirochete)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 20-Jun-2000

C;Accession: G71272

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin-
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDou-
ghey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A;Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.

A;Reference number: A71250; MUID:98332770; PMID:9665876

A;Accession: G71272

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-427 <COL>

A;Cross-references: GB:AE001256; GB:AE000520; NID:g3323171; PIDN:AAC65826.1; PID:g33231.1

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0863

C;Superfamily: nitrogen fixation protein nifs

C;Keywords: phosphoprotein; pyridoxal phosphate; sulfotransferase

F;23/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

F;374/Active site: Cys (cysteine persulfide intermediate) #status predicted

Query Match 2.5%; Score 7; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TGTRGRS 133
|||||
DB 166 TGTRGRS 172

RESULT 21

B84192

zinc metalloproteinase homolog [imported] - *Halobacterium* sp. NRC-1

C;Species: *Halobacterium* sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: B84192

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl-
Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L.

A;Title: Genome sequence of *Halobacterium* species NRC-1.

A;Reference number: B84160; MUID:20504483; PMID:11016950

A;Accession: B84192

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-428 <STO>

A;Cross-references: GB:AE004437; NID:g10579955; PIDN:AAG18905.1; GSPDB:GNO0138

C;Genetics:

A;Gene: caax

Query Match 2.5%; Score 7; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 SSRSGHS 162
|||||
DB 237 SSRSGHS 243

RESULT 22

B72109

GMP synthase CP0599 [imported] - *Chlamydia pneumoniae* (strains CWL029 and AR39)

C;Species: *Chlamydia pneumoniae*, *Chlamydia pneumoniae*

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C;Accession: B72109; B81558

R;Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.

Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: B72109

A;Molecule type: DNA

A;Residues: 1-429 <ARN>

A;Cross-references: GB:AE001604; GB:AE001363; NID:g4376438; PIDN:AAD18324.1; PID:g43764.

A;Experimental source: strain CWL029

R;Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: B81558
A:Molecule type: DNA
A:Residues: 1-429 <REA>
A:Cross-references: GB:AE002218; GB:AE002161; NID:g7189509; PIDN:AAF38415.1; PID:g718951
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: guaA; CP0599
C:Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology
P:11-194/Domain: trpG homology <TRG>

Query Match 2.5%; Score 7; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSQH 161
|||||
DB 248 ESSRSQH 254

RESULT 23
C86512
GMP synthase [imported] - Chlamydomophila pneumoniae (strain J138)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Aug-2001
C:Accession: C86512
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: C86512
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-429 <STO>
A:Cross-references: GB:BA000008; NID:g8978544; PIDN:BAA98381.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: guaA
C:Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology

Query Match 2.5%; Score 7; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSQH 161
|||||
DB 248 ESSRSQH 254

RESULT 24
AF2539
manganese transport protein all7601 [imported] - Nostoc sp. (strain PCC 7120) plasmid pC
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AF2539
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2539
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-442 <KUR>
A:Cross-references: GB:AF003602; PIDN:BAF77244.1; PID:g17134686; GSPDB:GN00181
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all7601
A:Genome: plasmid
C:Superfamily: natural resistance-associated macrophage protein 1

Query Match 2.5%; Score 7; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 56;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 LLOSLCV 31
|||||
DB 76 LLOSLCV 82

RESULT 25
T39359
probable udp-n-acetylglucosamine pyrophosphorylase - fission yeast (Schizosaccharomyce:
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T39359
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21848
A:Accession: T39359
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-475 <WOO>
A:Cross-references: EMBL:AL035675; PIDN:CAB38688.1; GSPDB:GN00067; SPDB:SPBCL289.08
A:Experimental source: strain 972h-; cosmid C1289
C:Genetics:
A:Gene: SPDB:SPBCL289.08
A:Map position: 2

Query Match 2.5%; Score 7; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETIS 101
|||||
DB 168 TSEETIS 174

RESULT 26
T19496
hypothetical protein C27A7.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
C:Accession: T19496
R:Harris, B.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19132
A:Accession: T19496
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-511 <WIL>
A:Cross-references: EMBL:Z81041; PIDN:CAB02786.1; GSPDB:GN00023; CESP:C27A7.2
A:Experimental source: clone C27A7
C:Genetics:
A:Gene: CESP:C27A7.2
A:Map position: 5
A:Introns: 44/3; 87/2; 130/2; 164/3; 203/2; 273/3; 325/1; 369/2
C:Superfamily: Caenorhabditis elegans hypothetical protein F07G11.3

Query Match 2.5%; Score 7; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 YKSGIA 55
|||||
DB 120 YKSGIA 126

RESULT 27
A47503
epoxide hydrolase (EC 3.3.2.3), cytosolic - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A47503; S17104; S19319
R:Knehr, M.; Thomas, H.; Arand, M.; Gebel, T.; Zeller, H.D.; Oesch, F.
J. Biol. Chem. 268, 17623-17627, 1993

A;Title: Isolation and characterization of a cDNA encoding rat liver cytosolic epoxide hydrolase
A;Reference number: A47503; MUID:93352557; PMID:8349641
A;Accession: A47503
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-554 <KNE>
A;Cross-references: GB:X65083; NID:9402631; PIDN:CAA46211.1; PID:9402632
A;Note: sequence extracted from NCBI backbone (NCBIN:136329, NCBIP:136330)
A;Experimental source: liver
R;Arand, M.; Knehr, M.; Thomas, H.; Zeller, H.D.; Oesch, F.
submitted to the EMBL Data Library, September 1991
A;Description: The unusual bicompartimental distribution of cytosolic epoxide hydrolase
A;Reference number: S17104
A;Accession: S17104
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 450-554 <ARA>
A;Cross-references: EMBL:X60328; NID:G55929; PIDN:CAA42898.1; PID:G55930
R;Arand, M.; Knehr, M.; Thomas, H.; Zeller, H.D.; Oesch, F.
FEBS Lett. 294, 19-22, 1991
A;Title: An impaired peroxisomal targeting sequence leading to an unusual bicompartimental
A;Reference number: S19319; MUID:92077134; PMID:1743286
A;Accession: S19319
A;Molecule type: mRNA
A;Residues: 448-554 <AR2>
C;Keywords: cytosol; ether hydrolase

Query Match 2.5%; Score 7; DB 2; Length 554;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 KALGRKI 151
DB 477 KALGRKI 483

RESULT 28
C82280
sensor kinase citA VC0791 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: C82280
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
charadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, B.
I, R.K.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82280
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-565 <HEI>
A;Cross-references: GB:AE004164; GB:AE003852; NID:G9655232; PIDN:AAF93956.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0791
A;Map position: 1
C;Superfamily: two-component sensor histidine kinase; sensor histidine kinase homology

Query Match 2.5%; Score 7; DB 2; Length 565;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 VIFTVLL 26
DB 185 VIFTVLL 191

RESULT 29
T22360
hypothetical protein F47G4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T22360
R;White, S.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z19553
A;Accession: T22360
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-710 <WIL>
A;Cross-references: EMBL:Z99171; PIDN:CAB16314.1; GSPDB:GN00019; CESP:F47G4.2
A;Experimental source: clone F47G4
C;Genetics:
A;Gene: CESP:F47G4.2
A;Map position: 1
A;Introns: 20/1; 131/3; 220/2; 273/1; 380/2; 577/2

Query Match 2.5%; Score 7; DB 2; Length 710;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 ILRTSEE 98
DB 647 ILRTSEE 653

RESULT 30
AE3032
conserved hypothetical protein Atu3866 [imported] - Agrobacterium tumefaciens (strain C)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AE3032
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCiel.
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreepan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE3032
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-801 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44675.1; PID:gl7742302; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu3866
A;Map position: linear chromosome

Query Match 2.5%; Score 7; DB 2; Length 801;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ASFFGAF 278
DB 216 ASFFGAF 222

RESULT 31
G98253
hypothetical protein AGR_L1958 [imported] - Agrobacterium tumefaciens (strain C58, Cer.
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: G98253
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G98253
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-801 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89553.1; PID:gl5159435; GSPDB:GN00170

```

C;Genetics:
A;Gene: AGR_L1958
A;Map position: linear chromosome

Query Match      2.5%; Score 7; DB 2; Length 801;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 ASFFGAF 278
    |||||
Db 216 ASFFGAF 222

RESULT 32
T20430
hypothetical protein E03A3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20430
R;Gardner, A.
submitted to the EMBL Data Library, October 1994
A;Reference number: Z19274
A;Accession: T20430
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-809 <MIL>
A;Cross-references: EMBL:Z38112; PIDN:CAA86232.1; GSPDB:GN00021; CESP:E03A3.2
A;Experimental source: clone E03A3
C;Genetics:
A;Gene: CESP:E03A3.2
A;Map position: 3
A;Introns: 49/3; 144/1; 319/2; 376/3; 484/2; 540/3; 573/2; 612/3; 720/3; 776/3

Query Match      2.5%; Score 7; DB 2; Length 809;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 EYGLYSI 242
    |||||
Db 756 EYGLYSI 762

RESULT 33
D90183
ATP-dependent helicase [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: D90183
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Feng, X.; Thi-Ngoc, H.P.; Redder, H.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90183
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-913 <KUR>
A;Cross-references: GB:AE006641; NID:g13813545; PIDN:AAK40723.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO0394

Query Match      2.5%; Score 7; DB 2; Length 913;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 ENDRIFV 258
    |||||
Db 517 ENDRIFV 523

RESULT 34
T15683
hypothetical protein C28C12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15683
R;Miller, N.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C28C12.
A;Reference number: Z18387
A;Accession: T15683
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-926 <MIL>
A;Cross-references: EMBL:U40797; NID:g1065916; PID:g1065927; PIDN:AAB37553.1; GSPDB:GN
A;Experimental source: strain Bristol N2; clone C28C12
C;Genetics:
A;Gene: CESP:C28C12.10
A;Map position: 4
A;Introns: 18/3; 98/2; 173/2; 206/3; 298/3; 405/3; 488/3; 727/3; 761/1; 828/2

Query Match      2.5%; Score 7; DB 2; Length 926;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 DEESMNS 75
    |||||
Db 122 DEESMNS 128

RESULT 35
JH0109
glycoprotein 14 precursor - equine herpesvirus 1
C;Species: equine herpesvirus 1
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 26-Aug-1999
C;Accession: JH0109
R;Guo, P.
Gene 87, 249-255, 1990
A;Title: Characterization of the gene and an antigenic determinant of equine herpesvir
A;Reference number: JH0109; MUID:90236317; PMID:1692002
A;Accession: JH0109
A;Molecule type: DNA
A;Residues: 1-979 <GUO>
A;Cross-references: GB:M34861; NID:g330900; PIDN:AAA46086.1; PID:g330901
A;Note: Glycoprotein 14 is homologous to corresponding glycoprotein of pseudorabies, b
C;Genetics:
A;Gene: gpi4
C;Superfamily: herpesvirus glycoprotein B
C;Keywords: glycoprotein; transmembrane protein
F;1-86/Domain: signal sequence #status predicted <SIG>
F;87-979/Product: glycoprotein 14 #status predicted <MAT>
F;831-871/Region: hydrophobic
F;165,275,380,423,497,514,560,727,749,951,970/Binding site: carbohydrate (Asn) (covalen

Query Match      2.5%; Score 7; DB 2; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 SGIACFL 58
    |||||
Db 839 SGIACFL 845

RESULT 36
E88465
protein B0244.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E88465
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biol
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_e
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; a

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A;Accession: E88465
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-382 <STO>
 A;Cross-references: GB:chr_III; PIDN:AAA68379.1; PID:G861359; GSPDB:GN00021; CESP:B0244.
 C;Genetics:
 A;Gene: B0244.6
 A;Map position: 3

Query Match 2.5%; Score 7; DB 2; Length 982;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RSNTLSS 138
 |||||
 DB 461 RSNTLSS 467

RESULT 37

T36031
 excinuclease ABC chain A SCC54.18c [similarity] - Streptomyces coelicolor
 N;Contains: excision endonuclease ABC (EC 3.1.1.-) chain A
 C;Species: Streptomyces coelicolor
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001
 R;Accession: T36031
 R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, March 1999
 A;Reference number: Z21581
 A;Accession: T36031
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1014 <SE>
 A;Cross-references: EMBL:AL035591; PIDN:CAB38148.1; GSPDB:GN00070; SCODEB:SCC54.18c
 A;Experimental source: strain A3(2)
 C;Genetics:
 A;Gene: uvrA; SCODEB:SCC54.18c
 C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
 C;Keywords: ATP; DNA binding; DNA repair; hydrolase; nucleotide binding; P-loop
 F;32-39/Region: nucleotide-binding motif A (P-loop)
 F;645-652/Region: nucleotide-binding motif A (P-loop)

Query Match 2.5%; Score 7; DB 2; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117
 |||||
 DB 153 SPLVRER 159

RESULT 38

T19214
 UDP-glucose-glycoprotein glucosyltransferase (EC 2.4.1.-) precursor F26H9.8 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T19214; T21444
 R;Barlow, K.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19091
 A;Accession: T19214
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1377 <W1>
 A;Cross-references: EMBL:Z81467; PIDN:CAB03874.1; GSPDB:GN00019; CESP:F26H9.8
 A;Experimental source: clone C12C8
 R;Baynes, C.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19422

A;Accession: T21444
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1377 <W12>
 A;Cross-references: EMBL:Z81516; PIDN:CAB04207.1; GSPDB:GN00019; CESP:F26H9.8

A;Experimental source: clone F26H9
 C;Genetics:
 A;Gene: CESP:F26H9.8
 A;Map position: 1

A;Introns: 40/2; 70/1; 152/2; 318/2; 429/3; 494/2; 538/3; 564/3; 625/3; 654/3; 782/3; 8;
 C;Keywords: Glycoprotein; glycosyltransferase; hexosyltransferase

Query Match 2.5%; Score 7; DB 2; Length 1377;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 NLHLRNG 172
 |||||
 DB 1014 NLHLRNG 1020

RESULT 39

T33236
 hypothetical protein T10H9.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T33236
 R;Greco, T.; Bradshaw, H.; O'Brien, D.
 submitted to the EMBL Data Library, May 1998
 A;Description: The sequence of C. elegans cosmid T10H9.
 A;Reference number: Z21306
 A;Accession: T33236
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1414 <GRE>
 A;Cross-references: EMBL:AF067949; PIDN:AAC19236.1; GSPDB:GN00023; CESP:T10H9.2
 A;Experimental source: strain Bristol N2; clone T10H9
 C;Genetics:
 A;Gene: CESP:T10H9.2
 A;Map position: 5
 A;Introns: 56/3; 76/1; 101/1; 161/1; 196/1; 226/3; 269/2; 318/1; 364/1; 475/3; 520/2; 5;

Query Match 2.5%; Score 7; DB 2; Length 1414;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 RGPORVA 123
 |||||
 DB 1110 RGPORVA 1116

RESULT 40

E64477
 replication factor C homolog - Methanococcus jannaschii
 C;Species: Methanococcus jannaschii
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C;Accession: E64477
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A.; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64300; MUID:96337999; PMID:8688087
 A;Accession: E64477
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-1847 <BUL>
 A;Cross-references: GB:U67583; GB:L77117; NID:G2826409; PIDN:AAB99433.1; PID:G1592072;
 C;Genetics:
 A;Map position: REV1393176-1387633
 A;Start codon: TTG

Query Match 2.5%; Score 7; DB 2; Length 1847;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 IFELKEN 253

hemagglutinin/hemolysin-related protein NM1779 [imported] - Neisseria meningitidis (strain 1809-1815)
C:Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C/Accession: G81044
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Hart, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Iri, H.; Qian, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A>Title: Sequence of the 3' half of the Murray Valley encephalitis virus genome and ma
A:Reference number: A60288; MUID:91102934; PMID:1702914
A:Accession: A60288
A:Molecule type: Genomic RNA
A:Residues: 1504-1778,'v',1780-3434 <LEE>

C;Genetics:
A;Gene: atp8
A;Genome: mitochondrion
A;Genetic code: SGC2
C;Superfamily: yeast H⁺-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; ox:

Query Match 2.1%; Score 6; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 IFTVLL 26
| | | | |
Db 19 IFTVLL 24

RESULT 48
AF2105
Hypothetical protein asl2397 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AF2105
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, T.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A;Reference number: AB1807; UID:21595285; PMID:11759840
A;Accession: AF2105
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-55 <R>
A;Cross-references: GB:BA000019; PIDN:BAB74096.1; PID:g1713489; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asl2397

C60157
 hypothetical protein 2 (prtM 5' region) - Lactococcus lactis subsp. cremoris plasmid pW
 C;Species: Lactococcus lactis subsp. cremoris
 C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 03-Feb-2003
 C;Accession: C60157
 R;Haandrikman, A.J.; van Leeuwen, C.; Kok, J.; Vos, P.; de Vos, W.M.; Venema, G.
 Appl. Environ. Microbiol. 56, 1890-1896, 1990
 A;Title: Insertion elements on lactococcal proteinase plasmids.
 A;Reference number: A60157; MUID:90343335; PMID:2166472
 A;Accession: C60157
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-56 <HAA>
 A;Cross-references: GB:M37396; NID:g149472; PIDN:AAA25212.1; PID:g149474
 C;Genetics:
 A;Genome: plasmid pW05

Query Match	2.1%;	Score 6;	DB 2;	Length 56;
Best Local Similarity	100.0%;	Pred. No. 1.1e+02;		
Matches	6;	Conservative 0;	Mismatches 0;	Indels 0;
QY	24	VLLQSL	29	
Db	39	VLLQSL	44	


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RESULT 50
C97621
hypothetical protein AGR_C3957 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C/Accession: C97621
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurolo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; MUID:21609551; PMID:11743194
A/Accession: C97621
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-62 <KUR>
A/Cross-references: GB:AE007869; PIDN:AAK87924.1; PID:gl5157324; GSPDB:GN00169
C/Genetics:
A/Gene: AGR_C3957
A/Map position: circular chromosome

Query Match          2.1%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 GPQKVA 123
      |||||
Db 7 GPQKVA 12

RESULT 51
AG0025
probable bacterioferritin-associated ferredoxin bfd [imported] - Yersinia pestis (strain
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
C/Accession: AG0025
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AG0025
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-64 <KUR>
A/Cross-references: GB:AL590842; PIDN:CAC89066.1; PID:gl5978306; GSPDB:GN00175
C/Genetics:
A/Gene: bfd
C/Superfamily: yheA protein

Query Match          2.1%; Score 6; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLRLV 88
      |||||
Db 28 QLRLV 33

RESULT 52
AC0774
hypothetical protein STY2363 [imported] - Salmonella enterica subsp. enterica serovar Ty
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: This species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AC0774
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
Sh, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
```

```
A/Accession: AC0774
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-65 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD02513.1; PID:gl503375; GSPDB:GN00176
C/Genetics:
A/Gene: STY2363

Query Match          2.1%; Score 6; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 IKENTK 201
      |||||
Db 46 IKENTK 51

RESULT 53
C91249
hypothetical protein ECs4963 [imported] - Escherichia coli (strain O157:H7, substrain
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C/Accession: C91249
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ge
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: C91249
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-85 <HAY>
A/Cross-references: GB:BA000007; PIDN:BAH38386.1; PID:gl3364439; GSPDB:GN00154
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: ECs4963

Query Match          2.1%; Score 6; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 EKOONI 110
      |||||
Db 31 EKOONI 36

RESULT 54
S78744
protein YDR363w-a - yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 19-Apr-2002
C/Accession: S78744
R/Du, Z.
submitted to the EMBL Data Library, June 1995
A/Description: The sequence of S. cerevisiae cosmid 9476.
A/Reference number: S61148
A/Accession: S78744
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-89 <DUZ>
A/Cross-references: EMBL:U28372; MIPS:YDR363w-a
C/Genetics:
A/Gene: SGD:HOD1
A/Cross-references: SGD:S0007235
A/Map position: 4R

Query Match          2.1%; Score 6; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 FTNELK 43
      |||||
Db 73 FTNELK 78
```

RESULT 55
B82311
conserved hypothetical protein VC0527 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C:Species: *Vibrio cholerae*
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: B82311
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.I.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82311
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <HEI>
A:Cross-references: GB:AE004139; GB:AE003852; NID:g9654953; PIDN:AAF93695.1; GSPDB:GN001139
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0527
A:Map position: 1
C:Superfamily: hypothetical protein HI0673

Query Match 2.1%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 NLHLRN 171
Db 47 NLHLRN 52
|||||

RESULT 56
AE3205
transposase tnp [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont) plasmid AT
C:Species: *Agrobacterium tumefaciens*
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AE3205
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelland, K.; Romero, P.; Zhang, S.
Science 294, 2317-2322, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE3205
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <KUR>
A:Cross-references: GB:AE008687; PIDN:AAL46059.1; PID:g17743819; GSPDB:GN00188
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: tnp
A:Genome: Plasmid

Query Match 2.1%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 LVRERG 118
Db 17 LVRERG 22
|||||

RESULT 57
G91248
hypothetical protein ECs4959 [imported] - *Escherichia coli* (strain O157:H7, substrain R1)
C:Species: *Escherichia coli*
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: G91248

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genome reference number: A99629; MUID:21156231; PMID:11258796
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G91248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <HAV>
A:Cross-references: GB:BA000007; PIDN:BA038382.1; PID:g13364435; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs4959

Query Match 2.1%; Score 6; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 SFGCAF 278
Db 15 SFGCAF 20
|||||

RESULT 58
C95337
probable cytochrome C fragment [imported] - *Sinorhizobium meliloti* (strain 1021) magap1.
C:Species: *Sinorhizobium meliloti*
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: C95337
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowler, S.; Kaiman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*.
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: C95337
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <KUR>
A:Cross-references: GB:AE006469; PIDN:AAK65261.1; PID:g14523712; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, H.; P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMall13
A:Genome: plasmid

Query Match 2.1%; Score 6; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 VAAHIT 127
Db 96 VAAHIT 101
|||||

RESULT 59
B69832
conserved hypothetical protein yhg8 - *Bacillus subtilis*.
N:Alternate names: hypothetical protein y (pbpF 5' region)
C:Species: *Bacillus subtilis*
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: B69832; C40614
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch. A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

Query Match 2.1%; Score 6; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 VAAHIT 127
Db 96 VAAHIT 101
|||||

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallex
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koether, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Muecel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A;Authors: Yoshikawa, H.P.; Zumbstein, E.; Yoshikawa, H.; Zanchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A;Reference number: A69580; MUID:98044033; PMID:9384377
 A;Accession: B69832
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-104 <KUN>
 A;Cross-references: GB:299109; GB:AL009126; NID:92633260; PIDN:CB12849.1; PID:el183011;
 A;Experimental source: strain 168
 R;Popham, D.L.; Setlow, P.
 J. Bacteriol. 175, 4870-4876, 1993
 A;Title: Cloning, nucleotide sequence, and regulation of the *Bacillus subtilis* pbpF gene
 A;Reference number: A40614; MUID:93328693; PMID:8335642
 A;Accession: C40614
 A;Molecule type: DNA
 A;Residues: 1-57 <POP>
 A;Cross-references: GB:L10630
 C;Genetics:
 A;Gene: yhgB

Query Match 2.1%; Score 6; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 LMKSR 227
 Db 25 LMKSR 30

RESULT 60
 B86818
 hypothetical protein ypiJ [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
 C;Species: *Lactococcus lactis* subsp. *lactis*
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C;Accession: B86818
 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ss
 A;Reference number: A86625; MUID:21235186; PMID:11337471
 A;Accession: B86818
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-105 <STO>
 A;Cross-references: GB:AE005176; PID:g12724547; PIDN:AAK05644.1; GSPDB:GN00146
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: ypiJ

Query Match 2.1%; Score 6; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 SSPNSK 142
 Db 42 SSPNSK 47

RESULT 61
 S09964
 Ig kappa chain V-J region (105-2H) - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 12-Feb-1993 #sequence_revision 13-Feb-1993 #text_change 21-Jan-2000
 C;Accession: S09964
 R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatou, J.C.; Izui, S.

Eur. J. Immunol. 20, 771-777, 1990
 A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibod
 A;Reference number: S09955; MUID:90269328; PMID:2347362
 A;Accession: S09964
 A;Molecule type: mRNA
 A;Residues: 1-107 <REI>
 A;Cross-references: EMBL:X51852; NID:955393; PIDN:CAA36145.1; PID:g930229
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 2.1%; Score 6; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 TISTVQ 104
 Db 74 TISTVQ 79

RESULT 62
 A44887
 Glucose transporter isoform 1, GLUT 1 - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 24-Sep-1999
 C;Accession: A44887
 R;Hogan, A.; Heyner, S.; Charron, M.J.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.;
 Development 113, 363-372, 1991
 A;Title: Glucose transporter gene expression in early mouse embryos.
 A;Reference number: A44887; MUID:92111400; PMID:1765007
 A;Accession: A44887
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-107 <HOG>
 A;Cross-references: GB:S77924; NID:g242127; PIDN:AAB20846.1; PID:g242128
 A;Experimental source: embryo
 A;Note: this sequence is inconsistent with the nucleotide translation
 A;Note: sequence extracted from NCBI backbone (NCBIN:77924, NCBI:P:77925)
 C;Superfamily: glucose transport protein

Query Match 2.1%; Score 6; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 IFTVLL 26
 Db 80 IFTVLL 85

RESULT 63
 F84012
 hypothetical protein BH2902 [imported] - *Bacillus halodurans* (strain C-125)
 C;Species: *Bacillus halodurans*
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C;Accession: F84012
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hi
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* an
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: F84012
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-109 <STO>
 A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA06621.1; GSPDB:GN
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH2902

Query Match 2.1%; Score 6; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 170 RNGELV 175

Db 38 RNGELV 43
|||||

RESULT 64

AC2887 conserved hypothetical protein Atu2526 [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AC2887

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:21608550; PMID:11743193

A:Accession: AC2887

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-112 <KUR>

A:Cross-references: GB:AE008688; PIDN:AAL43513.1; PID:g17741022; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu2526

A:Map position: circular chromosome

Query Match 2.1%; Score 6; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 HLRNGE 173
|||||

Db 35 HLRNGE 40

RESULT 65

H97662 hypothetical protein AGR_C_4590 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: H97662

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58

A:Reference number: A97359; PMID:21608551; PMID:11743194

A:Accession: H97662

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-112 <KUR>

A:Cross-references: GB:AB007869; PIDN:AAK88257.1; PID:g15157717; GSPDB:GN00169

C:Genetics:

A:Gene: AGR_C_4590

A:Map position: circular chromosome

Query Match 2.1%; Score 6; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 HLRNGE 173
|||||

Db 35 HLRNGE 40

RESULT 66

B25924 Ig kappa chain precursor V region (Ser-b) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000

A:Accession: B25924

R:Boyd, R.T.; Goldrick, M.M.; Gottlieb, P.D.

Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138, 1986
A:Title: Structural differences in a single gene encoding the V-kappa-Ser group of light chain (Ser-b) - mouse
A:Reference number: A94141; PMID:87067464; PMID:3097643
A:Accession: B25924

A:Molecule type: DNA

A:Residues: 1-115 <BOY>

A:Cross-references: GB:M14360; NID:g197464; PIDN:AAA39034.1; PID:g197465

A:Experimental source: strain BALB/c

C:Genetics:

A:Introns: 17/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Product: Ig kappa chain V region Ser-b #status predicted <MAT>

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 2.1%; Score 6; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 TISTVQ 104
|||||

Db 94 TISTVQ 99

RESULT 67

C83166

probable chaperone PA3842 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83166

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim

.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path

A:Reference number: A82950; PMID:20437337; PMID:10984043

A:Accession: C83166

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-116 <STO>

A:Cross-references: GB:AE004801; GB:AE004091; NID:g9950011; PIDN:AAG07229.1; GSPDB:GN00

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PA3842

C:Superfamily: Yersinia pestis plasmid pCD1 hypothetical protein syce

Query Match 2.1%; Score 6; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 PNDEES 72
|||||

Db 21 PNDEES 26

RESULT 68

F97174

hypothetical protein CAC2228 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: F97174

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee

.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.

A:Reference number: A96900; PMID:21359325; PMID:21359325

A:Accession: F97174

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-117 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK80185.1; PID:g15025227; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:
A;Gene: CAC2228

Query Match 2.1%; Score 6; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 171 NGELVI 176
Db 91 NGELVI 96

RESULT 69

JQ2032
lambda 208 protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus
C;Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpNPV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Accession: JQ2032

R;Russell, R.L.Q.; Rohrmann, G.F.

J. Gen. Virol. 74, 1191-1195, 1993
A;Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus
A;Reference number: PQ0633; MUID:93286576; PMID:8389803

A;Accession: JQ2032

A;Molecule type: DNA

A;Residues: 1-119 <RUS>

A;Cross-references: DBJ:DL3375; NID:G222217; PIDN:BAA02641.1; PID:G222223
C;Superfamily: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus lambda 208 pr

Query Match 2.1%; Score 6; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLRQLV 88
Db 90 QLRQLV 95

RESULT 70

D89803
conserved hypothetical protein SA0358 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C;Accession: D89803

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: D89803

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-122 <KUR>

A;Cross-references: GB:BA000018; PID:G13700285; PIDN:BA041583.1; GSPDB:GN00149

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA0358

Query Match 2.1%; Score 6; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 KEDDSY 64
Db 42 KEDDSY 47

RESULT 71

AH0043

Probable lipoprotein YPO0352 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C;Accession: AH0043

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Hoiden, M.T.G.; Prentice, M.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11596360

A;Accession: AH0043

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-128 <KUR>

A;Cross-references: GB:AL590842; PIDN:CAC89211.1; PID:G15978450; GSPDB:GN00175

C;Genetics:

A;Gene: YPO0352

C;Superfamily: Escherichia coli hypothetical protein o128

Query Match 2.1%; Score 6; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 SNTLSS 138
Db 35 SNTLSS 40

RESULT 72

D64559

hypothetical protein HP0316 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C;Accession: D64559

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,

A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: D64559

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-130 <TOM>

A;Cross-references: GB:AE000549; GB:AE000511; NID:G2313403; PIDN:AA007385.1; PID:G2313

Query Match 2.1%; Score 6; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 FTNELK 43
Db 111 FTNELK 116

RESULT 73

F86829

ribose ABC transporter permease protein rbsd [imported] - Lactococcus lactis subsp. la
C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C;Accession: F86829

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehr
Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: F86829

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-132 <STO>

A;Cross-references: GB:AE005176; PID:G12724648; PIDN:AAK05736.1; GSPDB:GN00146

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: rbsd

C;Superfamily: fucose operon U protein

Query Match 2.1%; Score 6; DB 2; Length 132;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 EBIKEN 199
|||||
DB 71 EBIKEN 76

RESULT 74
F70650
hypothetical protein RV3069 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: F70650
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70650
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-132 <COL>
A:Cross-references: GB:283866; GB:AL123456; NID:g3261691; PIDN:CAB06254.1; PID:g1781143
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV3069
C:Superfamily: hypothetical protein MJ1523

Query Match 2.1%; Score 6; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 GAFLVG 281
|||||
DB 48 GAFLVG 53

RESULT 75
AC0855
probable regulatory protein STY3045 [imported] - Salmonella enterica subsp. enterica ser
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0855
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0855
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD06026.1; PID:g16503993; GSPDB:GN00176
C:Genetics:
A:Gene: STY3045

Query Match 2.1%; Score 6; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 QLVKRM 91
|||||
DB 127 QLVKRM 132

Search completed: March 23, 2004, 09:24:14
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:16:30 ; Search time 18 seconds

(without alignments)
812.873 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MANMEVGGPSLGTCVLIV.....NEHLIDMDHEASFFGAFLVG 281

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size: 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database: SwissProt.42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	281	100.0	281	1	TN10_HUMAN
2	14	5.0	291	1	TN10_MOUSE
3	7	2.5	51	1	INS_ORNAN
4	7	2.5	81	1	VMD2_MOUSE
5	7	2.5	96	1	AH4_TOXGO
6	7	2.5	204	1	LIPE_NITEU
7	7	2.5	209	1	GEMI_HUMAN
8	7	2.5	240	1	CD7_HUMAN
9	7	2.5	362	1	YELJ_CABEL
10	7	2.5	420	1	SUN4_YEAST
11	7	2.5	442	1	MNTH_ANASP
12	7	2.5	475	1	UAP1_SCHPO
13	7	2.5	554	1	HVES_RAT
14	7	2.5	574	1	C306_DROME
15	7	2.5	670	1	YFGG_SCHPO
16	7	2.5	703	1	AT6B_HUMAN
17	7	2.5	979	1	VGLB_HSVEL
18	7	2.5	982	1	YS96_CABEL
19	7	2.5	1009	1	UVRA_STRAW
20	7	2.5	1014	1	UVRA_STRCO
21	7	2.5	1095	1	AT9B_HUMAN
22	7	2.5	1095	1	AT9B_MOUSE
23	7	2.5	1780	1	FOLG_MVEV
24	6	2.1	48	1	ATP8_SCHPO
25	6	2.1	67	1	RL29_METAC
26	6	2.1	67	1	RL29_METAC
27	6	2.1	94	1	FISB_VIBCH
28	6	2.1	96	1	IMMK_ECOLI
29	6	2.1	104	1	YHGB_BACSU
30	6	2.1	119	1	Y13K_NPVOP
31	6	2.1	126	1	ACPS_VIBPA
32	6	2.1	132	1	CRB1_MYCTU
33	6	2.1	137	1	YB47_SYNY3

34	6	2.1	143	1	B701_HSV6G
35	6	2.1	152	1	YE83_METJA
36	6	2.1	185	1	YAJ5_SCHPO
37	6	2.1	174	1	TN15_HUMAN
38	6	2.1	181	1	YE18_METJA
39	6	2.1	183	1	NLPC_HAEIN
40	6	2.1	184	1	UBC4_WHEAT
41	6	2.1	190	1	RL9_DROME
42	6	2.1	200	1	COAE_STRCO
43	6	2.1	209	1	GLOB_TOBAC
44	6	2.1	210	1	CYC4_AZOVI
45	6	2.1	220	1	RPOA_ASTLO
46	6	2.1	224	1	THY2_XENLA
47	6	2.1	227	1	THY1_XENLA
48	6	2.1	233	1	HIS3_THEMA
49	6	2.1	235	1	RGS1_HUMAN
50	6	2.1	236	1	UBL1_YEAST
51	6	2.1	238	1	F801_SCHMA
52	6	2.1	245	1	PDXJ_SHEON
53	6	2.1	247	1	THL1_ARATH
54	6	2.1	254	1	PSE3_HUMAN
55	6	2.1	257	1	OXAL_BACHD
56	6	2.1	260	1	FLGG_BUCBP
57	6	2.1	261	1	RL1_HSV2H
58	6	2.1	261	1	TNF5_AOTTR
59	6	2.1	261	1	TNF5_BOVIN
60	6	2.1	261	1	TNF5_CALJA
61	6	2.1	261	1	YKNA_CLOSA
62	6	2.1	262	1	CTE2_HUMAN
63	6	2.1	262	1	CTE2_MOUSE
64	6	2.1	262	1	YA23_METJA
65	6	2.1	267	1	YKU6_YEAST
66	6	2.1	272	1	TNF5_CHICK
67	6	2.1	273	1	DEFC_ARATH
68	6	2.1	279	1	DEFC_LYCES
69	6	2.1	282	1	KC2C_ARATH
70	6	2.1	283	1	DPH5_SCHPO
71	6	2.1	284	1	YNFH_ECOLI
72	6	2.1	285	1	LPXC_CHLVC
73	6	2.1	288	1	YHCS_HAEIN
74	6	2.1	291	1	EGC1_LISIN
75	6	2.1	291	1	EGC1_LISMO
76	6	2.1	296	1	NIH2_ANAVA
77	6	2.1	297	1	PANE_LISMO
78	6	2.1	299	1	Y025_MYCPN
79	6	2.1	304	1	XERD_COREF
80	6	2.1	306	1	PERE_ARMRU
81	6	2.1	307	1	YL72_ARCFU
82	6	2.1	313	1	YM8C_YEAST
83	6	2.1	313	1	Y940_METJA
84	6	2.1	318	1	YQAI_BACSU
85	6	2.1	322	1	FATB_VIBAN
86	6	2.1	322	1	YQAI_CABEL
87	6	2.1	323	1	YQAI_CABEL
88	6	2.1	323	1	YQAI_CABEL
89	6	2.1	329	1	YQAI_CABEL
90	6	2.1	329	1	YQAI_CABEL
91	6	2.1	329	1	YQAI_CABEL
92	6	2.1	330	1	YQAI_CABEL
93	6	2.1	333	1	LDHB_XENLA
94	6	2.1	334	1	T2D5_HAEIN
95	6	2.1	340	1	FMT_SCHPO
96	6	2.1	340	1	ILVC_CAMJE
97	6	2.1	340	1	LEU3_COREF
98	6	2.1	340	1	YF71_ARCFU
99	6	2.1	341	1	VSX1_CARAU
100	6	2.1	342	1	PURS_LACSK

ALIGNMENTS

RESULT 1

TN10 HUMAN
ID TN10 HUMAN STANDARD; PRT; 281 AA.
AC P50591;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
GN TNFSF10 OR TRAIL OR APO2L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=961111955; PubMed=8777713;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
RT family that induces apoptosis.";
RL Immunity 3:673-682(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96278649; PubMed=8663110;
RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
RA Ashkenazi A.;
RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
RT necrosis factor cytokine family.";
RL J. Biol. Chem. 271:12687-12690(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
RX MEDLINE=20017054; PubMed=10549288;
RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
RA Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
RT complex with death receptor 5.";
RL Mol. Cell 4:563-571(1999).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
RX PubMed=10542098;
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RA Jones E.Y., Screaton G.R.;
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT specificity in apoptotic initiation.";
RL Nat. Struct. Biol. 6:1048-1053(1999).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
RX MEDLINE=99413670; PubMed=10485660;
RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
RA Sung Y.C., Oh B.-H.;
RT "2.8 Å resolution crystal structure of human TRAIL, a cytokine with
RT selective antitumor activity.";
RL Immunity 11:253-261(1999).
CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC may be modulated by binding to the decoy receptors
CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC induce apoptosis.
CC -!- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
CC trimer.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
CC AND PROSTATE.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U37518; AAC50332.1; -;
CC EMBL; U57059; AAB01233.1; -;
CC EMBL; BC032722; AAH32722.1; -;
CC PDB; 1D0G; 22-OCT-99.
CC PDB; 1D4V; 01-NOV-99.
CC PDB; 1D2Q; 11-FEB-00.
CC PDB; 1DG6; 26-SEP-01.
CC Gene; HGNC:11925; TNFSF10.
CC MIM; 603598; -;
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005625; C: soluble fraction; TAS.
CC GO; GO:0005102; F: receptor binding; TAS.
CC GO; GO:0007267; F: cell-cell signaling; TAS.
CC GO; GO:0006917; P: induction of apoptosis; TAS.
CC GO; GO:0007165; P: signal transduction; TAS.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF-like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS00049; TNF 2; 1.
CC Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
CC Zinc; 3D-structure.
CC
CC DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC METAL 39 281 EXTRACELLULAR (POTENTIAL).
CC ZINC.
CC
CC DOMAIN 39 281
CC METAL 230 230
CC STRAND 123 127
CC TURN 130 131
CC TURN 137 139
CC STRAND 149 150
CC STRAND 163 165
CC STRAND 167 170
CC TURN 171 172
CC STRAND 173 176
CC STRAND 180 193
CC STRAND 205 213
CC STRAND 220 228
CC STRAND 237 250
CC TURN 252 253
CC STRAND 255 260
CC STRAND 263 265
CC HELIX


```

FT STRAND      266      267
FT TURN        270      272
FT STRAND      274      281
SQ SEQUENCE    281 AA; 32509 MW; DDAAAF78DAAB2F6D CRC64;

Query Match
Best Local Similarity 100.0%; Score 281; DB 1; Length 281;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEGGPSLGTCLVIFVTLQSLQVAVTVYVFTNELKQMDKYSKGIACFLKE 60
DB 1 MAMVEGGPSLGTCLVIFVTLQSLQVAVTVYVFTNELKQMDKYSKGIACFLKE 60
QY 61 DDSYWDNDESNMSPQWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDNDESNMSPQWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOBEIKENTKNDKQMVQIYKYTSYDPPILLMKSARNCSWSDAEVGLY 240
DB 181 FYIYSQTYFRFOBEIKENTKNDKQMVQIYKYTSYDPPILLMKSARNCSWSDAEVGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 2
TN10_MOUSE
ID TN10_MOUSE STANDARD; PRT; 291 AA.
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TNF10 protein).
GN TNFSF10 OR TRAIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT Identification and characterization of a new member of the TNF
RT family that induces apoptosis."
RL Immunity 3:673-682(1995).
CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC may be modulated by binding to the decoy receptors
CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC induce apoptosis.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: WIDESPREAD.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC EMBL; U37522; AAC52345.1; -.

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DR HSP; P50591; IDOG.
DR MGD; MGI:107414; Tnfsf10.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD00212; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.
FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 291;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKYTSYDPI 220
DB 217 VQYIYKYTSYDPI 230

RESULT 3
INS_ORNAN
ID INS_ORNAN STANDARD; PRT; 51 AA.
AC Q9TQY7; Q9TQY8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Insulin.
GN INS
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX NCBI_TaxID=9258;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=97021710; PubMed=8868070;
RA Nourse A., Treacy G.B., Shaw D.C., Jeffrey P.D.;
RT "Platypus insulin: indications from the amino acid sequence of
RT significant differences in structure from porcine insulin.";
RL Biol. Chem. Hoppe-Seyler 377:147-153(1996).
CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
CC increases cell permeability to monosaccharides, amino acids and
CC fatty acids. It accelerates glycolysis, the pentose phosphate
CC cycle, and glycogen synthesis in liver.
CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
CC disulfide bonds.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the insulin family.
CC FIR; S63591; S63590.
DR HSP; P01308; ILMJ.
DR InterPro; IPR004825; Ins/IGF/relax.
DR PRINTS; PR00277; INSULINB.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Glucose metabolism.
FT CHAIN 1 30 INSULIN B CHAIN.
FT NON_CONS 30 31
FT CHAIN 31 51 INSULIN A CHAIN.
FT DISULFID 7 37 INTERCHAIN.
FT DISULFID 19 50 INTERCHAIN.
FT DISULFID 36 41
SQ SEQUENCE 51 AA; 5854 MW; 0E4D30265D77EAA3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 178 EKGFFYY 184
DB 21 EKGFFYY 27

RESULT 4
VMD2 MOUSE
ID VMD2 MOUSE STANDARD; PRT; 81 AA.
AC O88870;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Bestrophin 1 (Vitellogenin macular dystrophy protein 2 homolog)
DE (Fragment)
GN VMD2 OR BMD1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98324772; PubMed=9662395;
RA Petukhin K., Kolesi M.G., Bakali B., Li W., Xie G., Marknell T.,
RA Sandgren O., Forsman K., Holmgren G., Andreasson S., Vujic M.,
RA Bergen A.A., McGarty-Dugan V., Figueroa D., Austin C.P., Metzker M.L.,
RA Caskey C.T., Wadelius C.;
RT "Identification of the gene responsible for Best macular dystrophy.";
RT Nat. Genet. 19:241-247(1998).
CC -!- FUNCTION: Forms calcium-sensitive chloride channels. May conduct
CC other physiologically significant anions such as bicarbonate (By
CC similarity).
CC -!- SUBUNIT: Tetramer or pentamers. May interact with PPP2CB and
CC PPP2R1B (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein; plasma membrane.
CC -!- PTM: Phosphorylated by PP2A (By similarity).
CC -!- SIMILARITY: Belongs to the bestrophin family.

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EMBL; AF057171; AAC64345.1; -.
DR MGD; MGI:1346332; Vmd2.
DR GO; GO:0016323; C:basolateral plasma membrane; ISS.
DR InterPro; IPR000615; Bestrophin.
DR Pfam; PF01062; Bestrophin; 1.
DR ProDom; PD002802; Worm fam.8; 1.
KW Transport; Ion transport; Ionic channel; Chloride channel; Chloride;
KW Calcium; Transmembrane; Phosphorylation.
FT NON_TER 1
FT NON_TER 81
FT NON_TER 81
SQ SEQUENCE 81 AA; 9413 MW; 19FD94AB3D606178 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 TVLLQSL 29
DB 27 TVLLQSL 33

RESULT 5
AH4_TOXGO
ID AH4_TOXGO STANDARD; PRT; 96 AA.
AC Q27001;
DT 01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Antigen H4 (Fragment).
GN H4.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH;
RX MEDLINE=91216437; PubMed=2022319;
RA Johnson A.M., Iilana S.;
RT "Cloning of Toxoplasma gondii gene fragments encoding diagnostic
RT antigens.";
RT Gene 99:127-132(1991).
CC
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CC
CC EMBL; M57302; AAA30139.1; -.
DR PIR; PS0423; PS0423.
KW Antigen.
FT NON_TER 1
FT CARBOHYD 34
FT CARBOHYD 34
SQ SEQUENCE 96 AA; 10853 MW; 69C7C2D14890FA53 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 192 FOEIKE 198
DB 2 FOEIKE 8

RESULT 6
LIPB NITEU
ID LIPB NITEU STANDARD; PRT; 204 AA.
AC Q82UJ6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lipocate-protein ligase B (EC 6.3.1.1) (lipocate biosynthesis protein
DE B).
GN LIPB OR NE1488.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RT J. Bacteriol. 185:2759-2773(2003).
CC -!- FUNCTION: Involved in the attachment of lipoyl groups to proteins,
CC by creating an amide linkage that joins the free carboxyl group of
CC lipolic acid to the epsilon-amino group of a specific lysine
CC residue in lipoylated proteins (By similarity).
CC -!- PATHWAY: Lipocate biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the lipB family.

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CC -----
 CC EMBL; BX321861; CAD85399.1; -
 CC HAMAP; MF 00013; -; 1.
 CC InterPro; IPR004143; BPL LipA LipB.
 CC InterPro; IPR000544; Lipotease_B.
 CC Pfam; PF03099; BPL LipA LipB; 1.
 CC ProDom; PD06086; Lipotease_B; 1.
 CC TIGRFAMs; TIGR00214; lipB; 1.
 CC PROSITE; PS01313; lipB; 1.
 CC KW Ligase; Complete proteome.
 CC SEQUENCE 204 AA; 22764 MW; A83F6E5F0346E61 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 RQLVRKM 91

DB 97 RQLVRKM 103

RESULT 7

GEMI_HUMAN

ID_GEMI_HUMAN STANDARD; PRT; 209 AA.

AC 075496; QSH1Z1;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Geminin.

GN GMN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98297356; PubMed=9635433;

RA McGarry T.J., Kirschner M.W.;

RT "Geminin, an inhibitor of DNA replication, is degraded during

RT mitosis.";

RL Cell 93:1043-1053 (1998).

RN [2]

RP SEQUENCE FROM N.A.

RA Corby N.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RX TISSUE=Lung and Urinary bladder;

RA MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner K.H., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Phney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Skalska U., Smalios D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- FUNCTION: Inhibits DNA replication by preventing the incorporation

CC of MCM complex into prereplication complex (pre-RC). It is

CC degraded during the mitotic phase of the cell cycle. Its

CC destruction at the metaphase-anaphase transition permits

CC replication in the succeeding cell cycle.

CC -1- DEVELOPMENTAL STAGE: Absent during G1 phase, accumulates during S,

CC G2, and M phases, and disappears at the time of the metaphase-

CC anaphase transition.

CC -1- SIMILARITY: Belongs to the geminin family.

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CC -----
 CC EMBL; AF067855; AAC39787.1; -
 CC EMBL; ALJ33264; CAC21511.1; ALT_INIT.
 CC EMBL; BC005185; AAH05185.1; -
 CC EMBL; BC005389; AAH05389.1; -
 CC Genew; HGNC:17493; GMN.

CC GK; 075496; -

CC GO; GO:0007050; P:cell cycle arrest; TAS.

CC GO; GO:0008156; P:negative regulation of DNA replication; TAS.

CC Cell cycle.

CC SEQUENCE 209 AA; 23565 MW; 0BABBE60F6F5AC252 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 209;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199

DB 9 QEEIKEN 15

RESULT 8

CD7_HUMAN

ID_CD7_HUMAN STANDARD; PRT; 240 AA.

AC P09564;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE T-cell antigen CD7 precursor (GP40) (T-cell leukemia antigen) (TP41)

DE (Leu-9).

GN CD7.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88111517; PubMed=3501369;

RA Aruffo A., Seed B.;

RT "Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a

RT COS cell expression system.";

RL EMBO J. 6:3313-3316 (1987).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91110576; PubMed=1703303;

RA Schanberg L.E., Fleener D.E., Kurtzberg J., Haynes B.F., Kaufman R.E.;

RT "Isolation and characterization of the genomic human CD7 gene:

RT structural similarity with the murine Thy-1 gene.";

RL Proc. Natl. Acad. Sci. U.S.A. 88:603-607 (1991).

RN [3]

RP SEQUENCE FROM N.A.

RX TISSUE=Muscle;

RL MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE OF 205-240 FROM N.A.
RX MEDLINE=91267564; PubMed=1711009;
RA Yoshikawa K., Seto M., Ueda R., Notake K., Yokochi T.,
RA Takahashi T.;
RT "Molecular cloning of the gene coding for the human T cell
RT differentiation antigen CD7";
RL Immunogenetics 33:352-360 (1991).
RN [5]
RP TOPOLOGY.
RX MEDLINE=90063052; PubMed=2479685;
RA Ware R.E., Searce R.M., Dietz M.A., Starmer C.F., Palker T.J.,
RA Haynes B.F.;
RT "Characterization of the surface topography and putative tertiary
RT structure of the human CD7 molecule";
RL J. Immunol. 143:3632-3640 (1989).
RN [6]
RP INTERACTION WITH SECTM1.
RX MEDLINE=20119303; PubMed=10652336;
RA Lyman S.D., Escobar S., Rousseau A.-M., Armstrong A., Fanslow W.C.;
RT "Identification of CD7 as a cognate of the human K12 (SECTM1)
RT protein";
RL J. Biol. Chem. 275:3431-3437 (2000).
CC -!- FUNCTION: Not yet known.
CC -!- SUBUNIT: Interacts with SECTM1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD7 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd7.htm".
CC -----
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CC -----
DR EMBL; X06180; CRA29546.1; -;
DR EMBL; M37271; AAA51953.1; -;
DR EMBL; BC009293; AAH09293.1; -;
DR EMBL; BC013297; AAH13297.1; -;
DR EMBL; D00749; BAA00646.1; -;
DR EMBL; D00747; BAA00646.1; JOINED.
DR EMBL; D00748; BAA00646.1; JOINED.
DR PIR; A39016; A39016.
DR HSP; P01607; IREI.
DR Genbank; HGNC:1695; CD7.
DR MIM; 168820; -;
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.

DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0042110; P:T-cell activation; TAS.
DR GO; GO:0007189; P:transmembrane receptor protein tyrosine kin. . .; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW T-cell; Signal; Immune response; Antigen; Transmembrane; Glycoprotein;
KW Immunoglobulin domain; Receptor; Lipoprotein; Palmitate; Repeat.
FT CHAIN 1 25
FT SIGNAL 26 240
FT DOMAIN 26 180
FT TRANSMEM 181 201
FT DOMAIN 202 240
FT DOMAIN 26 130
FT DOMAIN 145 180
FT DISULFID 35 142
FT DISULFID 48 114
FT LIPID 198 198
FT CARBOHYD 45 45
FT CARBOHYD 96 96
FT REPEAT 145 153
FT REPEAT 154 162
FT REPEAT 163 171
FT REPEAT 172 180
SQ SEQUENCE 240 AA; 25409 MW; EBBCE08279552108 CRC64;
Query Match 2.5%; Score 7; DB 1; Length 240;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 134 NTLSSPN 140
Db 231 NTLSSPN 237
|||||||
RESULT 9
YELJ CABEL
ID YELJ CABEL STANDARD; PRT; 362 AA.
AC P90756;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C27A7.2 in chromosome V.
GN C27A7.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Harris B.R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Durbin R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE DUF23 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z81041; CAB02786.2; -;
DR WormPep; C27A7.2; CE31886.
DR InterPro; IPR008166; DUF23.


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DR PFam: PF01566; Ntamp; 1.
DR PRINTS: PR00447; NATRESASCOMP.
DR ProDom: PD001861; Ntamp; 1.
DR TIGRFAMs: TIGR01197; ntamp; 1.
KW Transport; Symport; Manganese; Transmembrane; Inner membrane; Plasmid;
KW Complete proteome.
FT TRANSMEM 29 49 POTENTIAL.
FT TRANSMEM 62 82 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 135 155 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 209 229 POTENTIAL.
FT TRANSMEM 258 278 POTENTIAL.
FT TRANSMEM 295 315 POTENTIAL.
FT TRANSMEM 347 367 POTENTIAL.
FT TRANSMEM 372 392 POTENTIAL.
FT TRANSMEM 413 433 POTENTIAL.
SQ SEQUENCE 442 AA; 48418 MW; A7CBADFAE628196B CRC64;

Query Match 2.5%; Score 7; DB 1; Length 442;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 LIQSLCV 31
DB 76 LIQSLCV 82

RESULT 12
UAP1 SCHPO
ID UAP1 SCHPO STANDARD; PRT; 475 AA.
AC 094617;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23).
GN SPBC1289.08.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21849401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz B.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares K., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,
RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RC Nature 415:871-880(2002).
CC -!- CATALYTIC ACTIVITY: UTP + N-acetyl-alpha-D-glucosamine 1-phosphate

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CC = diphosphate + UDP-N-acetyl-D-glucosamine.
CC -!- PATHWAY: UDP-GlcNAc biosynthesis from Fru-6-P; fourth (last)
CC step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AL035675; CAB38688.1; -
CC PIR; T39359; T39359.
CC GeneDB SPombe; SPBC1289.08; -
CC InterPro; IPR002618; UDPGP.
CC Pfam; PF01704; UDPGP; 1.
CC Transferase; Nucleotidyltransferase.
FT SITE 106 106 BINDING SITE FOR GLCNAC-1-P (BY
FT ACT SITE 110 110 SIMILARITY).
FT ACT SITE 117 117 POTENTIAL.
SQ SEQUENCE 475 AA; 53121 MW; 3AF80295A682D7A3 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 TSEETIS 101
DB 168 TSEETIS 174

RESULT 13
HYES RAT
ID HYES RAT STANDARD; PRT; 554 AA.
AC P80299;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Soluble epoxide hydrolase (SEH) (EC 3.3.2.3) (Epoxide hydratase)
DE Cytosolic epoxide hydrolase (CEH).
GN EPHX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=93352557; PubMed=8349641;
RA Knehr M., Thomas H., Arand M., Gebel T., Zeller H.-D., Oesch F.;
RA "Isolation and characterization of a cDNA encoding rat liver
RA cytosolic epoxide hydrolase and its functional expression in
RA Escherichia coli."
RT J. Biol. Chem. 268:17623-17627(1993).
RL [2]
RP SEQUENCE OF 450-554 FROM N.A., AND PARTIAL SEQUENCE.
RN TISSUE=Liver;
RX MEDLINE=92077134; PubMed=1743286;
RA Arand M., Knehr M., Thomas H., Zeller H.-D., Oesch F.;
RA "An impaired peroxisomal targeting sequence leading to an unusual
RA bicompartamental distribution of cytosolic epoxide hydrolase."
RL FEBS Lett. 294:19-22(1991).
CC -!- FUNCTION: This enzyme acts on epoxides (alkene oxides, oxiranes)
CC and arene oxides. Plays a role in xenobiotic metabolism by
CC degrading potential toxic epoxides. Also determines steady-state
CC levels of physiological mediators.
CC -!- CATALYTIC ACTIVITY: An epoxide + H(2)O = a glycol.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and peroxisomal.
CC -!- INDUCTION: By compounds that cause peroxisome proliferation such

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as clofibrate, tiadenol and fenofibrate.
-!- SIMILARITY: Belongs to the AB hydrolase superfamily. Epoxide
hydrolase family.
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EMBL; X65083; CAA46211.1; -
EMBL; X60328; CAA42898.1; -
PIR; A47503.
HSP; P34914; 1CR6.
InterPro; IPR000073; A/b hydrolase.
InterPro; IPR003089; AB Hydrolase.
InterPro; IPR006639; Epox hydrolase.
InterPro; IPR006402; HAD-SF-IA-V3.
InterPro; IPR005833; Hlgnaase/hydrolase.
InterPro; IPR005834; Hydrolase.
InterPro; IPR000379; Ser esters.
Pfam; PF00561; abhydrolase; 1.
Pfam; PF00702; Hydrolase; 1.
PRINTS; PR00111; ABHYDROLASE.
PRINTS; PR00412; EPOXYHYDROLASE.
PRINTS; PR00413; HADHALOGNASE.
TIGRFAMs; TIGR01509; HAD-SF-IA-V3; 1.
Hydrolase; Peroxisome; Detoxification;
Aromatic hydrocarbons catabolism.
ACT_SITE 333 333 BY SIMILARITY.
ACT_SITE 495 495 BY SIMILARITY.
FT ACT_SITE 523 523 BY SIMILARITY.
FT ACT_SITE 552 554 BY SIMILARITY.
FT SITE 554 554 MICROBODY TARGETING SIGNAL (POTENTIAL).
SQ SEQUENCE 554 AA; 62340 MW; 145FDCAS3F592138 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 554;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 KALGRKI 151
DB 477 KALGRKI 483
|||||

RESULT 14
C306 DROME 2.5%; Score 7; DB 1; Length 574 AA.
ID _C306 DROME STANDARD; PRT; 574 AA.
AC Q3VWE5;
DR 16-OCT-2001 (Rel. 40, Created)
DR 16-OCT-2001 (Rel. 40, Last sequence update)
DR 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable cytochrome P450 306A1 (EC 1.14.-.-) (CYPCCVIAL).
GN CYP306A1 OR CG6578.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

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DE Hypothetical serine/threonine-rich protein C19G12.16c in chromosome I
DE precursor.

GN SPAC19G12.16C OR SPAC23A1.01C.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_taxid=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesti D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovsky G.V., Usery D., Barrell B.G., Nurse P.;

RA "The genome sequence of Schizosaccharomyces pombe.";

RL Nature 415:871-880(2002).

CC -!- SUBCELLULAR LOCATION: Secreted (Potential).

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CC EMBL; Z97209; CAB10128.1; ..

DR EMBL; AL021813; CAJ16975.1; ..

DR GeneDB Spombe; SPAC19G12.16c; ..

KW Hypothetical protein; Glycoprotein; Signal.

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

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FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

SQ SEQUENCE 670 AA; 68262 MW; 68E8D1CFB855F8A8 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 670;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 EETISTV 103

Db 584 EETISTV 590

RESULT 16

AT6B HUMAN

ID AT6B HUMAN STANDARD; PRT; 703 AA.

AC Q99941; Q13269; Q14343; Q14345; Q99635; Q9H3V9; Q9H3W1;

AC Q9NPL0;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cyclic-AMP-dependent transcription factor ATF-6 beta (Activating

DE transcription factor 6 beta) (ATF6-beta) (cAMP responsive element

DE binding protein-like 1) (cAMP response element binding protein-related

DE protein) (Creb-rp) (G13 protein).

GN CREBL1 OR G13

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Testis;

RX MEDLINE=96163866; PubMed=8586413;

RA Min J., Shukla H., Kozono H., Bronson S.K., Weissman S.M.,

RA Chaplin D.D.;

RT "A novel Creb family gene telomeric of HLA-DRA in the HLA complex.";

RL Genomics 30:149-156(1995).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=97024424; PubMed=8870652;

RA Khanna A., Campbell R.D.;

RT "The gene G13 in the class III region of the human MHC encodes a

RT potential DNA-binding protein.";

RL Biochem. J. 319:81-89(1996).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RA Rowen L., Danks C., Baskin D., Faust J., Loretz C., Ahearn M.E.,

RA Barta A., Schwartz S., Smith T.M., Spies T., Hood L.;

RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

RN [4]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=97081760; PubMed=8923003;

RA Speck M., Barry F., Miller W.L.;

RT "Alternate promoters and alternate splicing of human tenascin-X, a

RT gene with 5' and 3' ends buried in other genes.";

RL Hum. Mol. Genet. 15:1749-1758(1996).

RN [5]

RP SEQUENCE OF 158-700 FROM N.A.

RA Barlow K.;

RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RN [6]

RP CHARACTERIZATION.

RX MEDLINE=21157024; PubMed=11256944;

RA Haze K., Okada T., Yoshida H., Yanagi H., Yura T., Negishi M.,

RA Mori K.;

RT "Identification of the G13 (cAMP-response-element-binding

RT transcription factor 6) as a transcriptional activator of the

RT mammalian unfolded protein response.";

RL Biochem. J. 355:19-28(2001).

CC -!- FUNCTION: TRANSCRIPTIONAL FACTOR THAT ACTS IN THE UNFOLDED PROTEIN

CC RESPONSE (UPR) PATHWAY BY ACTIVATING UPR TARGET GENES INDUCED

CC DURING ER STRESS. BINDS DNA ON THE 5'-CCAC[GA]-3' HALF OF THE ER

CC STRESS RESPONSE ELEMENT (ERSE) (5'-CCAT-N9-CCAC[GA]-3') WHEN NF-Y

IS BOUND TO ERSE.

-!- SUBUNIT: HOMODIMER AND HETERODIMER WITH ATF6-ALPHA. THE DIMER INTERACTS WITH THE NUCLEAR TRANSCRIPTION FACTOR Y (NF-Y) TRIMER THROUGH DIRECT BINDING TO NF-Y SUBUNIT C (NF-YC).

-!- SUBCELLULAR LOCATION: Type II membrane protein in the endoplasmic reticulum. Under ER stress the cleaved N-terminal cytoplasmic domain translocates into the nucleus.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=2;

isoId=Q99941-1; Sequence=displayed;

Name=1;

isoId=Q99941-2; Sequence=VSP_000593;

Notes=No experimental confirmation available;

-!- TISSUE SPECIFICITY: Ubiquitous.

-!- DOMAIN: THE BASIC DOMAIN FUNCTIONS AS A NUCLEAR LOCALIZATION SIGNAL.

-!- DOMAIN: THE BASIC LEUCINE-ZIPPER DOMAIN IS SUFFICIENT FOR ASSOCIATION WITH THE NF-Y TRIMER AND BINDING TO ERSE.

-!- PTM: N-glycosylated.

-!- PTM: DURING UNFOLDED PROTEIN RESPONSE AN APPROXIMATIVE 60 KDA FRAGMENT CONTAINING THE CYTOPLASMIC TRANSCRIPTION FACTOR DOMAIN IS RELEASED BY PROTEOLYSIS. THE CLEAVAGE IS PROBABLY PERFORMED SEQUENTIALLY BY SITE-1 AND SITE-2 PROTEASES.

-!- SIMILARITY: Belongs to the bZIP family. ATF subfamily.

-!- CAUTION: SOME REF.4 SEQUENCES DIFFER FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 600.

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EMBL; U31903; AAA97438.1; -

EMBL; X98053; CAA66663.1; -

EMBL; X98054; CAA66664.1; -

EMBL; U89337; AAB47487.1; -

EMBL; U52694; AAG14900.1; -

EMBL; U52696; AAC50888.1; ALT FRAME.

EMBL; U52693; AAG14898.1; ALT_FRAME.

EMBL; U52701; AAC50883.1; ALT_SEQ.

EMBL; AL049547; CAB89295.1; -

Genew; HGNC:2349; CREBL1.

MIM; 600984; -

InterPro; IPR004827; TF_bZIP.

Pfam; PF00170; bZIP; 1.

PROSITE; PS50217; bZIP; 1.

PROSITE; PS00036; bZIP_BASIC; 1.

Transcription regulation; DNA-binding; Activator;

Unfolded protein response; Nuclear protein; Endoplasmic reticulum;

Transmembrane; Signal-anchor; Glycoprotein; Alternative splicing.

DOMAIN 1 396

TRANSMEM 397 417

DOMAIN 418 703

DOMAIN 1 86

DOMAIN BIND 327 347

DOMAIN 367 388

DOMAIN 96 105

SITE 410 410

SITE 413 413

SITE 440 441

SITE 476 476

CARBOHYD 505 505

CARBOHYD 610 610

CARBOHYD 627 627

CARBOHYD 676 676

VARSPLIC 28 31

GLQN -> D (in isoform 1).

FT CONFLICT 3 3 /FTIQ=VSP_000593.

FT CONFLICT 329 330 E -> D (IN REF. 2).

FT CONFLICT 520 520 QQ -> HE (IN REF. 2).

FT CONFLICT 600 600 V -> D (IN REF. 4; AAC50888).

FT CONFLICT 703 703 D -> G (IN REF. 1).

SQ SEQUENCE 703 AA; 76709 MW; B04C7B23E7D83F82 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 703;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TVLQSL 29

Db 265 TVLQSL 272

RESULT 17

VGLB_HSVEL STANDARD; PRT; 979 AA.

AC P25218;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Glycoprotein B precursor (Glycoprotein 14).

GN GB OR GP14 OR 33.

OS Equine herpesvirus type 1 (strain Kentucky D) (EHV-1).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Varicellovirus.

OX NCBI_TaxID=10330;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90236317; PubMed=1692002;

RA Guo P.;

RT "Characterization of the gene and an antigenic determinant of equine herpesvirus type-1 glycoprotein 14 with homology to gB-equivalent glycoproteins of other herpesviruses.";

RL Gene 87:249-255(1990).

CC -!- SIMILARITY: Belongs to the herpesviruses glycoprotein B family.

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EMBL; M34861; AAA46086.1; -

PIR; JH0109; JH0109.

InterPro; IPR000234; Glycoprot B.

Pfam; PF00606; Glycoprotein B; 1.

ProDom; PD000693; Glycoprot_B; 1.

Glycoprotein; Transmembrane; Signal.

SIGNAL 1 86

CHAIN 87 979

DOMAIN 87 851

TRANSMEM 852 869

DOMAIN 870 979

CYTOPLASMIC (POTENTIAL).

CARBOHYD 165 165

CARBOHYD 275 275

CARBOHYD 380 380

CARBOHYD 423 423

CARBOHYD 497 497

CARBOHYD 514 514

CARBOHYD 515 515

CARBOHYD 560 560

CARBOHYD 727 727

CARBOHYD 749 749

SEQUENCE 979 AA; 110331 MW; 9A19868B791C5B36 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 979;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      52 SGIA CFL 58
Db      |||||
      839 SGIA CFL 845

RESULT 18
YS96_CABEL YS96_CABEL STANDARD; PRT; 982 AA.
AC Q09965;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative G protein-coupled receptor B0244.6.
GN B0244.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Favello A.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Subfamily B0244.
CC -----
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CC -----
DR EMBL; U28971; AAA68379.1; -.
DR PIR; E88465; E88465.
DR WormPep; B0244.6; C501753.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Hypothetical protein; G-protein coupled receptor; Transmembrane;
KW Glycoprotein.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 208 228 POTENTIAL.
FT TRANSMEM 386 406 POTENTIAL.
FT TRANSMEM 430 450 POTENTIAL.
FT TRANSMEM 481 501 POTENTIAL.
FT TRANSMEM 648 668 POTENTIAL.
FT TRANSMEM 693 713 POTENTIAL.
FT TRANSMEM 813 833 POTENTIAL.
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 370 370 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 982 AA; 110441 MW; 4E88D46C74C940E CRC64;

Query Match 2.5%; Score 7; DB 1; Length 982;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      132 RSNTLSL 138
Db      |||||
      461 RSNTLSL 467

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RESULT 19
UVRA_STRAW UVRA_STRAW STANDARD; PRT; 1009 AA.
AC Q829X3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
GN UVRA OR SAV6286.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RA "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RA "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
CC -1- FUNCTION: The UvrABC repair system catalyzes the recognition and
CC processing of DNA lesions. UvrA is an ATPase and a DNA-binding
CC protein. A damage recognition complex composed of 2 uvrA and 2
CC uvrB subunits scans DNA for abnormalities. When the presence of a
CC lesion has been verified by uvrB, the uvrA molecules dissociate
CC (By similarity).
CC -1- SUBUNIT: Forms a heterotetramer with uvrB during the search for
CC lesions (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the ABC transporter family. UvrA subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP005046; BAC73997.1; -.
DR HAMAP; MF 00205; -.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR004602; UvrA.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC transporter; 1.
DR TIGRFAMs; TIGR00630; uvrA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
DR SOS response; Excision_nuclease; DNA repair; DNA recombination;
KW DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
KW Zinc-finger; Complete proteome.
FT NP_BIND 32 39 ATP (POTENTIAL).
FT NP_BIND 645 652 ATP (POTENTIAL).
FT ZN_FING 744 770 C4-TYPE.
SQ SEQUENCE 1009 AA; 110786 MW; CC90B4E219139700 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 1009;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117

| | | | |

Db 153 SPLVRER 159

RESULT 20

UVRA STRCO STANDARD; PRT; 1014 AA.

AC Q92507;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UVABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
GN UVRA OR SC01958 OR SCC54.18C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Gobie A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).

CC -1- FUNCTION: The UvrABC repair system catalyzes the recognition and
processing of DNA lesions. UvrA is an ATPase and a DNA-binding
protein. A damage recognition complex composed of 2 uvrA and 2
uvrB subunits scans DNA for abnormalities. When the presence of a
lesion has been verified by uvrB, the uvrA molecules dissociate
(By similarity).
CC -1- SUBUNIT: Forms a heterotrimer with uvrB during the search for
lesions (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the ABC transporter family. UvrA subfamily.

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or send an email to license@isb-sib.ch).

CC EMBL; AL939110; CAB38148.1; -.
DR PIR; T36031; T36031.
DR HAMAP; MF_0205; -; 1.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR004602; UvrA.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 1.
DR TIGRfams; TIGR00630; UvrA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW SOS response; Excision nuclease; DNA repair; DNA recombination;
KW DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
KW Zinc-finger; Complete proteome.
FT NP_BIND 32 39 ATP (POTENTIAL).
FT NP_BIND 645 652 ATP (POTENTIAL).
FT ZN_FING 744 770 C4-TYPE.
SQ SEQUENCE 1014 AA; 110997 MW; 084D6B18692A792D CRC64;

Query Match 2.5%; Score 7; DB 1; Length 1014;

RESULT 21

AT9B HUMAN STANDARD; PRT; 1095 AA.

AC O43861; O60872;
DT 30-MAY-2000 (Rel. 39, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Potential phospholipid-transporting ATPase IIB (EC 3.6.3.1) (HUSSY-
20).
GN ATP9B OR ATP11B OR NEOL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 1-420 FROM N.A.
RC TISSUE=Testis;
RA Ohshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Muraashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

CC [2]
RP SEQUENCE OF 208-1095 FROM N.A.
RA Birren B., Linton L., Nusbaum C., Lander E., Ali A., Allen N.,
RA Anderson S., Barna N., Bastien V., Boguslavskiy L., Boukhgalter B.,
RA Brown A., Camarata J., Campopiano A., Chang J., Chazaro B.,
RA Choepel Y., Collangelo M., Collins S., Collymore A., Cook A., Cooke P.,
RA DeArrellano K., Dewar K., Diaz J.S., Dodge S., Faro S., Ferreira P.,
RA Fitzhugh W., Gage D., Galagan J., Gardyna S., Ginde S., Gord S.,
RA Goyette M., Graham L., Grand-Pierre N., Hagos B., Heaford A.,
RA Horton L., Hulme W., Iliev I., Johnson R., Jones C., Kamat A.,
RA Karatas A., Kells C., LaRoque K., Lamazares R., Landers T.,
RA Lehoczyk J., Levine R., Liu G., MacLean C., Macdonald P., Major J.,
RA Marquis N., Matthews C., McCarthy M., McEwan P., McKernan K.,
RA McPheeters R., Meldrim J., Meneus L., Mihova T., Mienga V., Murphy T.,
RA Naylor J., Nguyen C., Norbu C., Norman C.H., O'Connor T.,
RA O'Donnell P., O'Neill D., Oliver J., Peterson K., Phunkhang P.,
RA Pierre N., Pollara V., Raymond C., Retta R., Rieback M., Riley R.,
RA Rise C., Rogov P., Roman J., Rosetti M., Roy A., Santos R.,
RA Schauer S., Schupbach R., Seaman S., Severy P., Spencer B.,
RA Strange-Thomann N., Stojanovic N., Strauss N., Subramanian A.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Travis N.,
RA Trigilio J., Vassiliev H., Viel R., Vo A., Wilson B., Wu X., Wyman D.,
RA Ye W.J., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

CC [3]
RP SEQUENCE OF 759-1095 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98217376; PubMed=9548971;
RA Halleck M.S., Pradhan D., Blackman C.F., Berkes C., Williamson P.L.,
RA Schlegel R.A.;
RT "Multiple members of a third subfamily of P-type ATPases identified by
genomic sequences and ESTs";
RL Genome Res. 8:354-361(1998).
RN [4]
RP SEQUENCE OF 768-1095 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21064499; PubMed=11124703;
RA Stanchi F., Bertocco E., Toppo S., Dioguardi R., Simionati B.,
RA Cannata N., Zimbello R., Lanfranchi G., Valle G.;

"Characterization of 16 novel human genes showing high similarity to yeast sequences";
 Yeast 18:69-80(2001).
 [5]
 RN CONCEPTUAL TRANSLATION.
 RA Axelsson K.B.;
 RP Unpublished observations (JUL-2002).
 RL -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
 CC
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 CC
 CC EMBL; AK097757; -; NOT ANNOTATED_CDS.
 DR EMBL; AC104423; -; NOT ANNOTATED_CDS.
 DR EMBL; U78978; AAC05243.1; -;
 DR EMBL; AJ006268; CAA06934.1; -;
 DR Genew; HGNC:13541; ATP9B.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0015247; F:aminophospholipid transporter activity; NAS.
 DR GO; GO:0005524; F:ATP binding; NAS.
 DR GO; GO:0019829; F:cation-transporting ATPase activity; NAS.
 DR GO; GO:0015917; P:aminophospholipid transport; NAS.
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR006539; Flippase.
 DR PRINTS; PR00119; CATATPASE.
 DR TIGRFAMs; TIGR01652; ATPase-Pilpid; 1.
 DR PROSITE; PS00154; ATPase_E1_E2; 1.
 KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding; Multigene family.
 FT DOMAIN 1 94
 FT TRANSMEM 95 116
 FT DOMAIN 117 121
 FT TRANSMEM 122 144
 FT DOMAIN 145 328
 FT TRANSMEM 329 349
 FT DOMAIN 350 357
 FT TRANSMEM 358 379
 FT DOMAIN 380 878
 FT TRANSMEM 879 899
 FT DOMAIN 900 911
 FT TRANSMEM 912 930
 FT DOMAIN 931 960
 FT TRANSMEM 961 979
 FT DOMAIN 980 986
 FT TRANSMEM 987 1009
 FT DOMAIN 1010 1015
 FT TRANSMEM 1016 1036
 FT DOMAIN 1037 1053
 FT TRANSMEM 1054 1078
 FT DOMAIN 1079 1095
 FT MOD_RES 416 416
 FT METAL 822 822
 FT METAL 826 826
 FT CONFLICT 834 834
 FT CONFLICT 954 954
 FT CONFLICT 968 968
 FT CONFLICT 984 984
 FT CONFLICT 1021 1021
 FT CONFLICT 1043 1043
 FT CONFLICT 1051 1051
 FT CONFLICT 1079 1079
 FT SEQUENCE 1095 AA; 123635 MW; 570C2E7DE507C255 CRC64;
 Query Match 2.5%; Score 7; DB 1; Length 1095;
 Best Local Similarity 100.0%; Pred. No. 58;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 241 SIYQGGI 247
 DB 968 SIYQGGI 974
 RESULT 22
 AT9B MOUSE
 ID AT9B MOUSE STANDARD; PRT; 1095 AA.
 AC P98155; O59LI3;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Potential phospholipid-transporting ATPase IIB (EC 3.6.3.1).
 GN ATP9B.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CN NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RX MEDLINE=20473714; PubMed=11015572;
 RA Hallett M.S., Lawler J.F. Jr., Blackshaw S., Gao L., Nagarajan P.,
 RA Hacker C., Pyle S., Newman J.F., Nakanishi Y., Ando H., Weinstein D.,
 RA Williamson P., Schlegel R.A.;
 RT "Differential expression of putative transbilayer amphipath
 RT transporters";
 RL Physiol. Genomics 1:139-150(1999).
 RN [2]
 RP SEQUENCE OF 658-1095 FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Found in most tissues except spleen and
 CC muscle. Most abundant in testis. Also detected in fetal tissues.
 CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-type
 CC ATPases). Subfamily IV.
 CC
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 CC
 CC EMBL; AF155913; AF08476.1; -;
 DR EMBL; BC003246; AA03246.1; -;
 DR MGD; MGI:1354757; At9B.
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR008250; E1-E2_ATPase_reg.


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FT DISULFID 295 322 BY SIMILARITY.
FT DISULFID 352 408 BY SIMILARITY.
FT DISULFID 366 397 BY SIMILARITY.
FT DISULFID 384 413 BY SIMILARITY.
FT DISULFID 482 580 BY SIMILARITY.
FT DISULFID 597 628 BY SIMILARITY.
FT DISULFID 797 808 BY SIMILARITY.
FT DISULFID 848 936
FT DISULFID 972 1016
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 923 923 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 968 968 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1000 1000 N-LINKED (GLCNAC. .) (HIGH MANNOSE).
FT NON_TER 1780 1780
SQ SEQUENCE 1780 AA; 194866 MW; OD6AA7FF0FB706DE CRC64;

Query Match 2.5%; Score 7; DB 1; Length 1780;
Best Local Similarity 100.0%; Pred.No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 VIFTVLL 26
DB 278 VIFTVLL 284

RESULT 24
ATP8_SCHPO
ID ATP8 SCHPO STANDARD; PRT; 48 AA.
AC P21536; Q9UUV72;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN ATP8.
OS Schizosaccharomyces pombe (Fission yeast).
OC Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=AD7-50;
RA Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 1-43 FROM N.A.
RC STRAIN=968 h90;
RX MEDLINE=20223868; PubMed=10759889;
RA Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
RA Hirooka Y.;
RT "Large-scale screening of intracellular protein localization in living
RT fission yeast cells by the use of a GFP-fusion genomic DNA library.";
RL Genes Cells 5:169-190(2000).
CC -!- FUNCTION: This is one of the chains of the nonenzymatic component
CC (CF0) subunit of the mitochondrial ATPase complex.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC H(+)(Out).
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- SIMILARITY: Belongs to the ATPase protein 8 family.
CC
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CC
CC EMBL; X54421; CAA38291.1; -.
DR EMBL; AB027775; BAA87079.1; -.

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KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 8 32 POTENTIAL.
SQ SEQUENCE 48 AA; 5636 MW; 36B3BF480A5FE803 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 48;
Best Local Similarity 100.0%; Pred.No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 IFTVLL 26
DB 19 IFTVLL 24

RESULT 25
RL29_METAC
ID RL29 METAC STANDARD; PRT; 67 AA.
AC Q8TRU0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L29P.
GN RPL29P OR MAl079.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=C2A / ATCC 35395 / DSM 2834;
RC MEDLINE=21929760; PubMed=11932338;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Smirnov S., Athnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McGowan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Heiderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Unyam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
CC -!- SIMILARITY: Belongs to the L29P family of ribosomal proteins.
CC
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CC
CC EMBL; AE010775; AAM04504.1; -.
DR HAVAP; MF 00374; -.
DR InterPro; IPR001854; Ribosomal L29.
DR Pfam; PF00831; Ribosomal L29; 1.
DR TIGRFAMs; TIGR00012; L29; 1.
DR PROSITE; PS00579; RIBOSOMAL L29; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 67 AA; 7612 MW; 232230E101E336B8 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 67;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 ILRTSE 97
DB 3 ILRTSE 8

RESULT 26

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RL29 METMA
ID _RL29_METMA STANDARD; PRT; 67 AA.
AC Q8PV43;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L29P.
GN RPL29P OR M2131.
OS Methanosaarcina mazei (Methanosaarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goei / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=21120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartisch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wieser A., Baesumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosaarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
CC -!- SIMILARITY: Belongs to the L29P family of ribosomal proteins.
CC -----
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CC -----
CC EMBL; AE013454; ANM31827.1; -
CC HAMAP; MF 00374; -; 1.
CC InterPro; IPR001854; Ribosomal L29.
CC Pfam; PF00831; Ribosomal_L29; 1.
CC TIGRFAMS; TIGR00012; L29; 1.
CC PROSITE; PS00579; RIBOSOMAL_L29; 1.
CC Ribosomal protein; Complete proteome.
SQ SEQUENCE 67 AA; 7612 MW; 232324E450A236B8 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 ILRTSE 97
Db 3 ILRTSE 8

RESULT 27
FTSB_VIBCH STANDARD; PRT; 94 AA.
AC Q9KUJ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cell division protein ftsB.
GN FTSB OR VC0527.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

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RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RL cholerae";
RN Nature 406:477-483(2000).
RP CHARACTERIZATION.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=21980622; PubMed=11972052;
RA Buddelmeijer N., Judson N., Boyd D., Mekalanos J.J., Beckwith J.;
RT "YgbQ, a cell division protein in Escherichia coli and Vibrio
RT cholerae, localizes in codependent fashion with FtsL to the division
RT site.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:6316-6321(2002).
CC -!- FUNCTION: Required for the cell division process.
CC -!- SUBUNIT: May interact with ftsL (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
CC (potential). Colocalizes with ftsL to the division site (By
CC similarity).
CC -!- SIMILARITY: Belongs to the ftsB family.
CC -----
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CC -----
CC EMBL; AS004139; AAF93695.1; ALT_INIT.
CC PIR; B82311; B82311.
CC TIGR; VC0527; -
CC HAMAP; MF 00599; -; 1.
CC InterPro; IPR007060; DivIC.
CC Pfam; PF04977; DivIC; 1.
CC Cell division; Transmembrane; Inner membrane; Coiled coil;
CC Complete proteome.
FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 4 21 POTENTIAL.
FT DOMAIN 22 94 PERIPLASMIC (POTENTIAL).
FT DOMAIN 32 76 COILED COIL (POTENTIAL).
FT SEQUENCE 94 AA; 10987 MW; CE7DF6651369821D CRC64;

Query Match 2.1%; Score 6; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 NLHLRN 171
Db 45 NLHLRN 50

RESULT 28
IMWK_ECOLI STANDARD; PRT; 96 AA.
AC Q47503; Q46784; Q47501;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Colicin K immunity protein.
GN CKI OR CFI.
OS Escherichia coli.
OG Plasmid ColK-K235.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K49, and ECOR5;
RX MEDLINE=96074330; PubMed=7592493;
RA Pilel H., Braun V.;
RT "Strong function-related homology between the pore-forming colicins K

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RT J. Bacteriol. 177:6973-6977 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Izard J., Chartier M., Baty D.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: THIS PROTEIN IS ABLE TO PROTECT A CELL, WHICH HARBORS
CC THE PLASMID COLK ENCODING COLICIN K, AGAINST COLICIN K.
CC -----
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CC -----
DR EMBL; X87834; CA661100.1; -
DR EMBL; X87835; CA661103.1; -
DR EMBL; U27452; AAB41289.1; -
KW Bacteriocin immunity; Plasmid; Transmembrane; Inner membrane.
FT TRANSMEM 73 POTENTIAL.
SQ SEQUENCE 96 AA; 11498 MW; E82853239597A5CD CRC64;

Query Match 2.1%; Score 6; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 IKENTK 201
DB 55 IKENTK 60

RESULT 29
YHGB BACSU
ID YHGB BACSU STANDARD; PRT; 104 AA.
AC P38048;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein yhgB.
GN YHGB OR BSU10090.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=982040224; PubMed=9579061;
RA Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.,
RA Wedler H., Venema G., Bron S.;
RT "The 172 kb prkA-addAB region from 83 degrees to 97 degrees of the
RT Bacillus subtilis chromosome contains several dysfunctional genes,
RT the glyB marker, many genes encoding transporter proteins, and the
RT ubiquitous hit gene."
RL Microbiology 144:859-875 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Barbero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

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RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekoweka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Yamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256 (1997).
RN [3]
RP SEQUENCE OF 1-67 FROM N.A.
RC STRAIN=168;
RX MEDLINE=93328693; PubMed=8335642;
RA Popham D.L., Setlow P.;
RT "Cloning, nucleotide sequence, and regulation of the Bacillus
RT subtilis pbpF gene, which codes for a putative class A
RT high-molecular-weight penicillin-binding protein."
RT J. Bacteriol. 175:4870-4876 (1993).
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CC -----
DR EMBL; Y14083; CAA74515.1; -
DR EMBL; Y29109; CAB12849.1; -
DR EMBL; L10630; AAA71940.2; -
DR PIR; E69832; E69832.
DR Subtilist; BG10426; yhgB.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 104 AA; 11998 MW; 6B44CD77B52PD968 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 LMKSR 227
DB 25 LMKSR 30

RESULT 30
Y13K NPVOP
ID Y13K NPVOP STANDARD; PRT; 119 AA.
AC Q05122;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hypothetical 13.4 kDa protein in ubiquitin 3'region (Lambda 208).
OS Orygia pseudotsugata multicapsid polyhedrosis virus (OpNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OX NCBI_TaxID=164623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93286576; PubMed=8389803;
RA Russell R.L.Q., Rohrmann G.F.;
RT "Nucleotide sequence of the ubiquitin-39K gene region from the Orygia
RT pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."
RL J. Gen. Virol. 74:1191-1195 (1993).
CC -----

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CC EMBL; D13375; BAA02641.1; -
 CC PIR; JQ2032; JQ2032.
 CC KW Hypothetical protein.
 CC SQ SEQUENCE 119 AA; 13415 MW; 8B35F990F5BD9678 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QLRLV 88
 Db 90 QLRLV 95
 |||||

RESULT 31

ACPS VIBPA STANDARD; PRT; 126 AA.
 AC Q87L3; 2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Holo-[acyl-carrier protein] synthase (SC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN ACPS OR VP2568.
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=670;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=RM2 2210633 / Serotype O3:K6;
 RX MEDLINE=22508454; PubMed=12620739;
 RA Makino K., Oshima K., Nakokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Najima M., Kurokawa M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
 RT distinct from that of *V. cholerae*.";
 RL Lancet 361:743-749(2003).
 CC [-] FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 CC A to a Ser of acyl-carrier protein (By similarity).
 CC [-] CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3', 5'-bisphosphate + holo-[acyl-carrier protein].
 CC [-] COPACTOR: Magnesium (By similarity).
 CC [-] SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC [-] SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 CC family.

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CC EMBL; AP005082; BAC60831.1; -
 CC HAMAP; MF 00101; -; 1.
 CC DR InterPro; IPR008278; 4-PPT_transf.
 CC DR Pfam; PF01648; ACPS; 1.
 CC KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
 CC Complete proteome.
 CC FT METAL 9 9 MAGNESIUM (BY SIMILARITY).
 CC FT METAL 58 58 MAGNESIUM (BY SIMILARITY).
 CC SQ SEQUENCE 126 AA; 13645 MW; C565E0E2812C3A3C CRC64;

Query Match 2.1%; Score 6; DB 1; Length 126;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 EKALGR 149
 Db 17 EKALGR 22
 |||||

RESULT 32

CRBL MYCTU STANDARD; PRT; 132 AA.
 AC P95089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein crCB homolog 1.
 GN CRBL OR RV3069 OR MT3153.1 OR MTCY22D7.12C OR MB3096.
 OS Mycobacterium tuberculosis, and
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773, 1765;
 RN [1]

RP SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
 RX MEDLINE=22206494; PubMed=12218036;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
 RT "Whole-genome comparison of *Mycobacterium tuberculosis* clinical and
 RT laboratory strains.";
 RL J. Bacteriol. 184:5479-5490(2002).
 RN [3]

RP SEQUENCE FROM N.A.
 RC SPECIES=M.bovis; STRAIN=AF2122/97;
 RX MEDLINE=22709107; PubMed=12788972;
 RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
 RA Pryor M., Duchey S., Grondin S., Lacroix C., Monsemp C., Simon S.,
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
 RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
 RT "The complete genome sequence of *Mycobacterium bovis*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
 CC [-] SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC [-] SIMILARITY: Belongs to the crCB family.

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CC EMBL; Z83866; CAB06254.1; -
 CC EMBL; AE007132; AAK47489.1; -.

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DR EMBL; BX248344; CAD96783.1; -.
DR PIR; F70650; F70650.
DR TIGR; MT3153.1; -.
DR TubercuList; RV3069; -.
DR HAMAP; MF_00454; -.
DR InterPro; IPR003691; Camphor_Crb.
DR Pfam; PF02537; CRCB; 1.
KW Transmembrane; Complete proteome.
FT TRANSMEM 9 31 POTENTIAL.
FT TRANSMEM 35 57 POTENTIAL.
FT TRANSMEM 70 92 POTENTIAL.
FT TRANSMEM 102 124 POTENTIAL.
SQ SEQUENCE 132 AA; 14301 MW; C49B283379B0174E CRC64;

Query Match          2.1%; Score 6; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 GAFLVG 281
Db 48 GAFLVG 53

RESULT 33
YB47_SNNY3
AC P73795; STANDARD; PRT; 137 AA.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein sll1147.
GN Sll1147.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A. PubMed=8905231;
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuura A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the MAPEG family.
CC -----
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CC -----
DR EMBL; D90309; BRA17849.1; -.
DR PIR; S74888; S74888.
DR InterPro; IPR001129; MAPEG.
DR Pfam; PF01124; MAPEG; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 5 25 POTENTIAL.
FT TRANSMEM 79 99 POTENTIAL.
FT TRANSMEM 109 129 POTENTIAL.
SQ SEQUENCE 137 AA; 15414 MW; 9741232427529924 CRC64;

Query Match          2.1%; Score 6; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 WQLRQL 87

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Db 129 WQLRQL 134

RESULT 34
B701_HSV6G
AC P30024; STANDARD; PRT; 143 AA.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcriptional regulatory protein B701.
OS Human herpesvirus (type 6 / strain GS) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10369;
RN [1]
RP SEQUENCE FROM N.A. PubMed=1310766;
RX MEDLINE=92148942; PubMed=1310766;
RA Geng Y., Chandran B., Josephs S.F., Wood C.;
RA "Identification and characterization of a human herpesvirus 6 gene
RA segment that trans activates the human immunodeficiency virus type 1
RA promoter.";
RT J. Virol. 66:1564-1570(1992).
CC -!- FUNCTION: MAY BE RESPONSIBLE FOR MOST OF THE TRANS-ACTIVATING
CC ACTIVITY ON THE HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 PROMOTER BY
CC HHV-6. IT MAY FUNCTION BY DIRECTLY BINDING TO THE NF-KAPPAB
CC SITE OR MAY INVOLVE CELLULAR FACTORS, SUCH AS NF-KAPPAB, EITHER
CC DIRECTLY OR INDIRECTLY.
CC -----
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CC -----
DR EMBL; M81789; -; NOT ANNOTATED_CDS.
DR PIR; A42186; WMBE6H.
KW Transcription regulation; Trans-acting factor; Activator.
SQ SEQUENCE 143 AA; 16385 MW; D0CE4D7C2422AAD8 CRC64;

Query Match          2.1%; Score 6; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 ISTVQE 105
Db 110 ISTVQE 115

RESULT 35
YB83_METJA
AC Q58878; STANDARD; PRT; 152 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein M31483.
GN M31483.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

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RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii".
 RL Science 273:1058-1073(1996).
 CC -----
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 CC -----
 CC EMBL; U67589; AAB99498.1; --
 DR PIR; B64485; B64485.
 DR TIGR; MJ1483; --
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 7 POTENTIAL.
 SQ SEQUENCE 152 AA; 17659 MW; 90227132448E8802 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 KNEKAL 147
 |||||
 Db 120 KNEKAL 125

RESULT 36
 YAU5 SCHPO STANDARD; PRT; 165 AA.
 ID YAJ5 SCHPO STANDARD; PRT; 165 AA.
 AC Q09905;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adaptin complex small chain homolog C3OD11.05.
 GN SPAC30D11.05.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hanlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger S., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grynoprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Farnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey P., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe".
 RL Nature 415:871-880(2002).
 CC -!- SIMILARITY: Belongs to the adaptor complexes small subunit
 CC family.
 CC -----

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 CC -----

CC EMBL; Z67961; CAA91891.1; --
 DR PIR; T38594; S62563.
 DR GeneDB Spombe; SPAC30D11.05; --
 DR InterPro; IPR000804; Clat adaptor s.
 DR Pfam; PF01217; Clat adaptor s; 1.
 DR PROSITE; PS00989; CLAT ADAPTOR S; 1.
 KW Hypothetical protein; Coated pits
 SQ SEQUENCE 165 AA; 18642 MW; 9EA796AD34C40FF3 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSS 138
 |||||
 Db 155 SNTLSS 160

RESULT 37
 TN15 HUMAN STANDARD; PRT; 174 AA.
 ID TN15 HUMAN STANDARD; PRT; 174 AA.
 AC Q95150;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 15 (Vascular
 DE endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
 GN TNFSF15 OR VEGI OR TLI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Umbilical vein;
 RX MEDLINE=99091541; PubMed=9872942;
 RA Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
 RA Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
 RA Li L.-Y., Gentz R., Yu G.-L.;
 RT "VEGI, a novel cytokine of the tumor necrosis factor family, is an
 RT angiogenesis inhibitor that suppresses the growth of colon carcinomas
 RT in vivo".
 RL FASEB J. 13:181-189(1999).
 CC -!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
 CC (in vitro).
 CC -!- SUBUNIT: Homotrimer (Potential).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
 CC Detected in placenta, lung, kidney, skeletal muscle, pancreas,
 CC spleen, prostate, small intestine and colon.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC -----

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CC EMBL; AF039390; AAD08783.1; -
DR HSP; P50591; 1D0G.
DR Genew; HGNC:11931; TNFSF15.
DR MIM; 604052; -
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0005102; F: receptor binding; TAS.
DR GO; GO:0000074; P: regulation of cell cycle; TAS.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytochrome, Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT DOMAIN 26 174 EXTRACELLULAR (POTENTIAL).
FT DISULFID 85 125 POTENTIAL.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 174 AA; 20131 MW; CCH83BA7EE673B98 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 PFGAFL 279
Db 168 PFGAFL 173

RESULT 38
YE18_METJA STANDARD; PRT; 181 AA.
AC Q58813;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical aldolase class II protein MJ1418.
GN MJ1418.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=9637999; PubMed=868087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.P., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073 (1996).
CC -!- COFACTOR: Binds 1 zinc ion per molecule (Potential).
CC -!- SIMILARITY: Belongs to the aldolase class II family. Arab/fuca
CC subfamily.
CC
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CC
CC EMBL; U67582; AAB99428.1; -
DR PIR; A64477; A64477.
DR HSP; P11550; 1DZX.
DR TIGR; MJ1418; -
DR InterPro; IPR001303; Aldolase_II_N.
DR Pfam; PF00596; Aldolase_II; 1.
KW Hypothetical protein; Zinc; Complete proteome.
FT METAL 68 87 ZINC (BY SIMILARITY).
FT METAL 87 87 ZINC (BY SIMILARITY).
FT METAL 89 89 ZINC (BY SIMILARITY).
FT METAL 147 147 ZINC (BY SIMILARITY).
SQ SEQUENCE 181 AA; 20470 MW; E5F3BF13722145B0 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 FLKEDD 62
Db 45 FLKEDD 50

RESULT 39
NLPC_HAEIN STANDARD; PRT; 183 AA.
AC P45296;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable lipoprotein nlpc homolog precursor.
GN NLPC OR H11652.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512 (1995).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Probable).
CC -!- SIMILARITY: BELONGS TO THE E. COLI NLPC / LISTERIA P60 FAMILY.
CC
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DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Membrane; Lipoprotein; Signal; Complete proteome; Palmitate.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 183 PROBABLE LIPOPROTEIN NLPC HOMOLOG.
 FT LIPID 18 18 N-palmitoyl cysteine (Potential).
 FT LIPID 18 18 S-diacylglycerol cysteine (Potential).
 SQ SEQUENCE 183 AA; 20585 MW; 772BB57F79452E38 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 LGRKIN 152
 Db 121 LGRKIN 126

RESULT 40
 UBC4_WHEAT
 ID UBC4_WHEAT STANDARD; PRT; 184 AA.
 AC P16577;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ubiquitin-conjugating enzyme E2-23 kDa (EC 6.3.2.19)
 DE (Ubiquitin-conjugating ligase) (Ubiquitin carrier protein).
 GN UBC4.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Augusta;
 RX MEDLINE=9009364; PubMed=2557633;
 RA Sullivan M.L., Vierstra R.D.;
 RT "A ubiquitin carrier protein from wheat germ is structurally and
 RT functionally similar to the yeast DNA repair enzyme encoded by
 RT RAD6.";
 RL J. Biol. Chem. 266:23878-23885(1991).
 RN [2]
 RP PROC. NATL. ACAD. SCI. U.S.A. 86:9861-9865(1989).
 RN [2]
 RP MUTAGENESIS OF CYS-85.
 RX MEDLINE=92084684; PubMed=1660887;
 RA Sullivan M.L., Vierstra R.D.;
 RT "Cloning of a 16-kDa ubiquitin carrier protein from wheat and
 RT Arabidopsis thaliana. Identification of functional domains by in
 RT vitro mutagenesis.";
 RL J. Biol. Chem. 266:23878-23885(1991).
 CC -1- FUNCTION: Catalyzes the covalent attachment of ubiquitin to other
 CC proteins.
 CC -1- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
 CC diphosphate + protein N-ubiquityllysine.
 CC -1- PATHWAY: Ubiquitin conjugation; second step.
 CC -1- MISCELLANEOUS: A cysteine residue is required for ubiquitin-
 CC thiolester formation.
 CC -1- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
 CC
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 CC
 CC EMBL; M28059; AAA34309.1; -
 CC PIR; A34506; A34506.
 CC HSP; Q95044; 2E2C.
 CC InterPro; IPR000608; UBQ_conjugat.
 CC Pfam; PF00179; UQ_con; 1.
 CC ProDom; PD000461; UBQ_conjugat; 1.
 CC SMART; SM00212; UBCc; 1.

DR PROSITE; PS00183; UBIQUITIN_CONJUGAT 1; 1.
 DR PROSITE; PS0127; UBIQUITIN_CONJUGAT 2; 1.
 KW Ub1 conjugation pathway; Ligase; Multigene family.
 FT BINDING 85 85 UBIQUITIN.
 FT DOMAIN 141 176 ASP/GLU-RICH (ACIDIC).
 FT MUTAGEN 85 85 C->S: LOSS OF ACTIVITY.
 SQ SEQUENCE 184 AA; 21125 MW; AA479C4B42C893B7 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 SIYQGG 246
 Db 42 SIYQGG 47

RESULT 41
 RL9_DROME
 ID RL9_DROME STANDARD; PRT; 190 AA.
 AC P50882; Q9VKL6; Q9VKL7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 60S ribosomal protein L9.
 GN RPL9 OR M(2)32D OR CG6141.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ganton-S.
 RX MEDLINE=96262132; PubMed=8676882;
 RA Schmidt A., Hollmann M., Schaefer U.;
 RT "A newly identified Minute locus, M(2)32D, encodes the ribosomal
 RT protein L9 in Drosophila melanogaster.";
 RL Mol. Gen. Genet. 251:381-387(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Paulis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.C.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Fertaz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpn G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Wellesbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RN REVISIONS.
 RP MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kinkler J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 FT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 CC -!- SIMILARITY: Belongs to the L6p family of ribosomal proteins.
 CC -----
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 CC -----
 DR EMBL; X94613; CAA64319.1; -;
 DR EMBL; AE003630; AAF53048.2; -;
 DR PIR; JC6062; JC6062.
 DR FlyBase; FBgn0015756; RPL9.
 DR InterPro; IPR000702; Ribosomal L6.
 DR InterPro; IPR002359; Ribosomal L6_2.
 DR Pfam; PF00347; Ribosomal L6; 2.
 DR PROSITE; PS00700; RIBOSOMAL_L6_2; 1.
 KW Ribosomal protein.
 FT CONFLICT 37 37 S -> T (IN REF. 1).
 SQ SEQUENCE 190 AA; 21392 MW; 689B2520ACDA12D3 CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 190;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 126 ITGTRG 131
 Db 27 ITGTRG 32
 RESULT 42
 COAE STRCO STANDARD; PRT; 200 AA.
 AC Q952K7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase).
 GN COAE OR SC01996 OR SC7H2.10C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Reil S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RL coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -!- FUNCTION: Catalyzes the phosphorylation of the 3'-hydroxyl group
 CC of dephosphocoenzyme A to form coenzyme A (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + dephospho-CoA = ADP + CoA.
 CC -!- PATHWAY: Coenzyme A (CoA) biosynthesis; fifth (last) step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the coae family.
 CC -----
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 CC -----
 DR EMBL; AL939111; CAB52052.1; -;
 DR PIR; T35741; T35741.
 DR HAMAP; MF_00376; -; 1.
 DR InterPro; IPR001977; Depp_CoAkinase.
 DR Pfam; PF01121; Coae; 1.
 DR ProDom; PD003329; Depp_CoAkinase; 1.
 DR TIGRFAMs; TIGR00152; TIGR00152; 1.
 DR PROSITE; PS01294; COAE; 1.
 KW Transferrase; Kinase; ATP-binding; Coenzyme A biosynthesis;
 KW Complete proteome.
 FT NP BIND 8 15
 SQ SEQUENCE 200 AA; 15500 MW; FC2F5151EBEF33AE CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 200;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 112 PLVRR 117
 Db 89 PLVRR 94
 RESULT 43
 GLOB TOBAC STANDARD; PRT; 209 AA.
 AC Q03416;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein GLOBOSA.
 GN GLO.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. SR1; TISSUE=Flower;
 RX MEDLINE=93288002; PubMed=8099711;
 RA Hansen G., Estruch J.J., Sommer H., Spena A.;
 RT "NTGLO: a tobacco homologue of the GLOBOSA floral homeotic gene of
 RL Antirrhinum majus: cDNA sequence and expression pattern.";
 RL Mol. Gen. Genet. 239:310-312(1993).
 CC -!- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH DEFICIENS (DEFA).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: EXPRESSED MAINLY IN FLORAL ORGANS AND, WITHIN
 CC THE FLOWER, EXPRESSION IS RESTRICTED TO PETALS AND STAMENS.
 CC -!- MISCELLANEOUS: MUTATIONS IN GLO CAUSE TRANSFORMATION OF PETALS

CC INTO SEALS AND STAMINA INTO CARPELS.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 CC -----
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 CC -----
 CC EMBL; X67959; CAA48142.1; --
 CC PIR; S35226; S35226.
 CC HSSP; P11746; 1MNM.
 CC TRANSFAC; T01779; --
 CC InterPro; IPR002487; TF_Kbox.
 CC InterPro; IPR002100; TF_MADSbox.
 CC Pfam; PF01486; K-box; 1.
 CC Pfam; PF00319; SRP-TF; 1.
 CC PRINTS; PR00404; MADSDOMAIN.
 CC SMART; SM00432; MADS; 1.
 CC PROSITE; PS00350; MADS_BOX_1; 1.
 CC PROSITE; PS00666; MADS_BOX_2; 1.
 CC Transcription regulation; DNA-binding; Activator; Nuclear protein;
 CC Developmental protein.
 CC DOMAIN 3 57 MADS-box.
 CC FT DOMAIN 91 163 K-BOX.
 CC SQ SEQUENCE 209 AA; 24691 MW; 5661F9C1640E1A47 CRC64;
 CC -----
 CC Query Match 2.1%; Score 6; DB 1; Length 209;
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 82 WQLRQL 87
 CC Db 160 WQLRQL 165
 CC -----
 CC RESULT 44
 CC CYC4 AZOVI
 CC ID_CVC4 AZOVI STANDARD; PRT; 210 AA.
 CC AC P43302;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Cytochrome C4 precursor.
 CC GN CYCA.
 CC OS Azotobacter vinelandii.
 CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC OC Pseudomonadaceae; Azotobacter.
 CC OX NCBI_TaxID=354;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=CA;
 CC RX MEDLINE=95345104; PubMed=7619830;
 CC RA Ng T.C.N., Laheri A.N., Maier R.J.;
 CC RT "Cloning, sequencing, and mutagenesis of the cytochrome c4 gene from
 CC RT Azotobacter vinelandii: characterization of the mutant strain and a
 CC RT proposed new branch in the respiratory chain.";
 CC RL Biochim. Biophys. Acta 1230:119-129(1995).
 CC RN [2]
 CC RP SEQUENCE OF 21-210.
 CC RC STRAIN=ATCC 13705 / OPI;
 CC RX MEDLINE=84307416; PubMed=6089759;
 CC RA Ambler R.P., Daniel M., Mellis K., Stout C.D.;
 CC RT "The amino acid sequence of the dihaem cytochrome c4 from the
 CC RT bacterium Azotobacter vinelandii.";
 CC RL Biochem. J. 222:217-227(1984).
 CC CC -1- FUNCTION: DIHEME, HIGH POTENTIAL CYTOCHROME C BELIEVED TO BE AN
 CC INTERMEDIATE ELECTRON DONOR TO TERMINAL OXIDATION SYSTEMS.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- PTM: Binds 2 heme groups per molecule.

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 CC -----
 CC EMBL; L37290; AAA87314.1; --
 CC PIR; I39740; I39740.
 CC HSSP; Q52369; LETF.
 CC InterPro; IPR008169; Cyt_C_bact.
 CC InterPro; IPR003088; Cyt_CI.
 CC InterPro; IPR008168; Cyt_CIC.
 CC InterPro; IPR000345; CytC_heme_BS.
 CC Pfam; PF00034; cytochrome_C_1.
 CC PRINTS; PR00605; CYTOCHROME_C_1.
 CC PRODOM; PD004020; Cyt_C_bact; 2.
 CC PROSITE; PS00190; CYTOCHROME_C; 2.
 CC KW Electron transport; Heme; Periplasmic; Signal.
 CC FT SIGNAL 1 20
 CC CHAIN 21 210 CYTOCHROME C4.
 CC BINDING 34 34 HEME 1 (COVALENT).
 CC BINDING 37 37 HEME 1 (COVALENT).
 CC METAL 38 38 IRON (HEME 1 AXIAL LIGAND).
 CC METAL 86 86 IRON (HEME 1 AXIAL LIGAND).
 CC BINDING 139 139 HEME 2 (COVALENT).
 CC BINDING 142 142 HEME 2 (COVALENT).
 CC METAL 143 143 IRON (HEME 2 AXIAL LIGAND).
 CC METAL 187 187 IRON (HEME 2 AXIAL LIGAND).
 CC SQ SEQUENCE 210 AA; 21687 MW; 4B09C4AA90D1FC74 CRC64;
 CC -----
 CC Query Match 2.1%; Score 6; DB 1; Length 210;
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 42 LKQMQD 47
 CC Db 61 LKQMQD 66
 CC -----
 CC RESULT 45
 CC RPOA ASTLO
 CC ID RPOA ASTLO STANDARD; PRT; 220 AA.
 CC AC P34778; P58144;
 CC DT 01-FEB-1994 (Rel. 28, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (PEP) (Plastid-
 CC DE encoded RNA polymerase alpha subunit) (RNA polymerase alpha subunit).
 CC GN RPOA.
 CC OS Astasia longa (Euglenophyceae alga).
 CC OG Chloroplast.
 CC OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
 CC OX NCBI_TaxID=3037;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=CCAP 1204-17a;
 CC RX MEDLINE=95163124; PubMed=7859309;
 CC RA Gockel G., Hachtel W., Baier S., Fliess C., Henke M.;
 CC RT "Genes for components of the chloroplast translational apparatus are
 CC RT conserved in the reduced 73-kb plastid DNA of the nonphotosynthetic
 CC RT euglenoid flagellate Astasia longa.";
 CC RL Curt. Genet. 36:256-262(1994).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=CCAP 1204-17a;
 CC RX MEDLINE=21080522; PubMed=11212895;
 CC RA Gockel G., Hachtel W.;
 CC RT "Complete gene map of the plastid genome of the nonphotosynthetic
 CC RT euglenoid flagellate Astasia longa.";
 CC RL Protist 151:347-351(2000).

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RN RP IDENTIFICATION OF GENE.
RA MEDLINE=21851312; PubMed=11861918;
RA Shevelova E.V., Giordani N.V., Hallick R.B.;
RT "Identification and comparative analysis of the chloroplast
RT alpha-subunit gene of DNA-dependent RNA polymerase from seven Euglena
RT species.";
RL Nucleic Acids Res. 30:1247-1254 (2002).
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA] (N).
CC -!- SUBUNIT: In chloroplasts the minimal PPV RNA polymerase is
CC composed of four subunits: alpha, beta, beta', and beta'' (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- SIMILARITY: Belongs to the RNA polymerase alpha chain family.
CC -!- CAUTION: Ref.1 and Ref.2 sequences differ from that shown due to
CC erroneous gene model prediction.
CC -!- CAUTION: The C-terminal domain thought to be required for
CC interaction with some regulatory factors is missing from this
CC protein.
CC
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CC
CC EMBL; AJ294725; CAC24589.1; ALT_SEQ.
CC EMBL; AJ294725; CAC24588.1; ALT_SEQ.
CC F1R; S38600; S38600.
CC HAMAP; MF 00059; atypical; 1.
CC InterPro; IPR009025; RBP1-like RNAPo.
CC InterPro; IPR001700; RNA pol. bac. org.
CC Transferrase; Transcription; DNA-directed RNA polymerase; Chloroplast.
CC SEQUENCE 220 AA; 26287 MW; D221F70D995BB5AB CRC64;

Query Match 2.1%; Score 6; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 BEIKEN 199
Db 84 BEIKEN 89

RESULT 46
THY2_XENLA
ID THY2_XENLA STANDARD; PRT; 224 AA.
AC Q00643;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thyroliberin precursor 2 (thyrotropin releasing hormone) (TRH).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92164783; PubMed=1537407;
RA Bulant M., Richter K., Kuchler K., Kreil G.;
RT "A cDNA from brain of Xenopus laevis coding for a new precursor of
RT thyrotropin-releasing hormone.";
RL FEBS Lett. 296:292-296 (1992).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: This precursor contains seven copies of

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thyroliberin.
CC -!- MISCELLANEOUS: There are at least two genes for TRH in Xenopus.
CC
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CC
CC EMBL; X64056; CAA45412.1; --
CC F1R; S20382; S20382.
CC InterPro; IPR008857; TRH.
CC F1R; PF05438; TRH; 1.
CC Amidation; Hormone; Repeat; Signal;
CC Cleavage on pair of basic residues; Multigene family;
CC Pyroglutamate carboxylic acid.
FT SIGNAL 1 15 BY SIMILARITY.
FT CHAIN 16 224 PROTHYROLIBERIN 2.
FT PEPTIDE 75 77 THYROLIBERIN.
FT PEPTIDE 89 91 THYROLIBERIN.
FT PEPTIDE 105 107 THYROLIBERIN.
FT PEPTIDE 119 121 THYROLIBERIN.
FT PEPTIDE 151 153 THYROLIBERIN.
FT PEPTIDE 166 168 THYROLIBERIN.
FT PEPTIDE 191 193 THYROLIBERIN.
FT MOD_RES 75 75 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 77 77 AMIDATION (G-78 PROVIDE AMIDE GROUP).
FT MOD_RES 89 89 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 91 91 AMIDATION (G-92 PROVIDE AMIDE GROUP).
FT MOD_RES 105 105 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT MOD_RES 119 119 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 121 121 AMIDATION (G-122 PROVIDE AMIDE GROUP).
FT MOD_RES 151 151 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 153 153 AMIDATION (G-154 PROVIDE AMIDE GROUP).
FT MOD_RES 166 166 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 168 168 AMIDATION (G-169 PROVIDE AMIDE GROUP).
FT MOD_RES 191 191 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 193 193 AMIDATION (G-194 PROVIDE AMIDE GROUP).
SQ SEQUENCE 224 AA; 26148 MW; 5F65114D5169BF15 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 RFQEEI 196
Db 80 RFQEEI 85

RESULT 47
THY1_XENLA
ID THY1_XENLA STANDARD; PRT; 227 AA.
AC P01152;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thyroliberin precursor 1 (thyrotropin releasing hormone) (TRH).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=90307692; PubMed=1694847;
RA Kuchler K., Richter K., Tirovsky J., Egger R., Kreil G.;
RT "Two precursors of thyrotropin-releasing hormone from skin of Xenopus
RT laevis. Each contains seven copies of the end product.";
RL J. Biol. Chem. 265:11731-11733 (1990).

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[2]
 RP SEQUENCE OF 1-123 FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=84182535; PubMed=6425056;
 RA Richter K., Kawashima E., Egger R., Kreil G.;
 RT "Biosynthesis of thyrotropin releasing hormone in the skin of Xenopus
 RL laevis: partial sequence of the precursor deduced from cloned cDNA.";
 EMBO J. 3:617-621(1984).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: This precursor contains seven copies of
 CC thyroliberin.
 CC -1- MISCELLANEOUS: There are at least two genes for TRH in Xenopus.
 CC
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 CC
 DR EMBL; M34699; AAA49973.1; -;
 DR EMBL; M34698; AAA49974.1; -;
 DR EMBL; X00770; CAA25345.1; ALT_TERM.
 DR PIR; A37061; RHXLIT.
 DR InterPro; IPR008857; TRH.
 DR Pfam; PF05438; TRH; 1.
 DR Annotation; Hormone; Repeat; Signal;
 KW Cleavage on pair of basic residues; Multigene family;
 KW Pyroglutamate carboxylic acid.
 FT SIGNAL 1 15
 FT CHAIN 16 227 PROTHYROLIBERIN 1.
 FT PEPTIDE 75 227
 FT PEPTIDE 75 227
 FT PEPTIDE 89 91 THYROLIBERIN.
 FT PEPTIDE 107 109 THYROLIBERIN.
 FT PEPTIDE 121 121 THYROLIBERIN.
 FT PEPTIDE 123 123 THYROLIBERIN.
 FT PEPTIDE 153 155 THYROLIBERIN.
 FT PEPTIDE 168 170 THYROLIBERIN.
 FT PEPTIDE 193 195 THYROLIBERIN.
 FT MOD_RES 75 75 PYROGLUTAMATE CARBOXYLIC ACID.
 FT MOD_RES 77 77 AMIDATION (G-78 PROVIDE AMIDE GROUP).
 FT MOD_RES 89 89 PYROGLUTAMATE CARBOXYLIC ACID.
 FT MOD_RES 91 91 AMIDATION (G-92 PROVIDE AMIDE GROUP).
 FT MOD_RES 107 107 PYROGLUTAMATE CARBOXYLIC ACID.
 FT MOD_RES 109 109 AMIDATION (G-110 PROVIDE AMIDE GROUP).
 FT MOD_RES 121 121 PYROGLUTAMATE CARBOXYLIC ACID.
 FT MOD_RES 123 123 AMIDATION (G-124 PROVIDE AMIDE GROUP).
 FT MOD_RES 153 153 PYROGLUTAMATE CARBOXYLIC ACID.
 FT MOD_RES 155 155 AMIDATION (G-156 PROVIDE AMIDE GROUP).
 FT MOD_RES 168 168 PYROGLUTAMATE CARBOXYLIC ACID.
 FT MOD_RES 170 170 AMIDATION (G-171 PROVIDE AMIDE GROUP).
 FT MOD_RES 193 193 PYROGLUTAMATE CARBOXYLIC ACID.
 FT MOD_RES 195 195 AMIDATION (G-196 PROVIDE AMIDE GROUP).
 FT VARIANT 46 46 L -> S.
 FT VARIANT 70 70 M -> I.
 FT VARIANT 218 220 MISSING.
 SQ SEQUENCE 227 AA; 26336 MW; 7DEC001E3154CD47 CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 191 RFQEEI 196
 Db 80 RFQEEI 85
 RESULT 48
 HIS9 THEM9 STANDARD; PRT; 233 AA.
 ID HIS9 THEM9
 AC Q9WZRI;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Probable histidinol-phosphatase (EC 3.1.3.15) (HolPase).
 GS HISK OR TM0804
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RL genome sequence of Thermotoga maritima";
 Nature 399:323-329(1999).
 CC -1- CATALYTIC ACTIVITY: L-histidinol-phosphate + H(2)O = L-histidinol
 CC + phosphate.
 CC -1- PATHWAY: Histidine biosynthesis; eighth step.
 CC -1- SIMILARITY: BELONGS TO THE PHP FAMILY OF HYDROLASE. HISK FAMILY.
 CC
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 CC
 DR EMBL; AE001748; AAD35886.1; -;
 DR PIR; E72330; E72330.
 DR TIGR; TM0804; -;
 DR InterPro; IPR004013; PHP_C.
 DR InterPro; IPR003141; PHP_N.
 DR Pfam; PF02811; PHP_C; 1.
 DR Pfam; PF02231; PHP_N; 1.
 DR SMART; SM00481; POLIITAC; 1.
 DR Histidine biosynthesis; Hydrolase; Complete proteome.
 KW SEQUENCE 233 AA; 27144 MW; E0CE3D245E0EDA30 CRC64;
 SQ
 Query Match 2.1%; Score 6; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 142 KNEKAL 147
 Db 153 KNEKAL 158
 RESULT 49
 RGS1 HUMAN
 ID RGS1_HUMAN STANDARD; PRT; 235 AA.
 AC Q9NS28;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Regulator of G-protein signaling 18 (RGS18).
 GN RGS18 OR RGS13.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang W., Wan T., Yuan Z., He L., Cao X.;
 RT "A novel regulator of G-protein signaling.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Platelet;

RA Gagnon A.W., Murray D.L., Leadley R.J. Jr.;
 RT "Cloning and characterization of a novel regulator of G-protein
 RL signaling in human platelets";
 RN Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 EX PubMed-11042171;
 RA Park I.K., Klug C.A., Li K., Jerabek L., Li L., Nanamori M.,
 RA Neubig R.R., Hood L., Weissman I.L., Clarke M.F.;
 RT "Molecular cloning and characterization of a novel regulator of
 RT G-protein signaling from mouse hematopoietic stem cells";
 RL J. Biol. Chem. 276:915-923(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. BINDS TO G(I)-ALPHA AND G(Q)-ALPHA
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in peripheral leukocytes, bone
 CC marrow, spleen and fetal liver.
 CC -1- SIMILARITY: Contains 1 RGS domain.
 CC -----
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 CC -----
 DR EMBL; AF076642; AAF80227.1; -.
 DR EMBL; AF268036; AAK58589.1; -.
 DR EMBL; BC020632; AAK20632.1; -.
 DR HSSP; P49799; IAGR.
 DR Genew; HGNC:14261; RGS18.
 DR MIM; 607192;
 DR InterPro; IPR000342; Regl_Gprotein.
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGSPTROTEIN.
 DR ProDom; PD001580; Regl_Gprotein; 1.
 DR SMART; SM00315; RGS; 1-
 DR PROSITE; PS00132; RGS; 1.
 KW Signal transduction inhibitor.
 FT DOMAIN 86 202 RGS.
 FT CONFLICT 226 227 DV -> ML (IN REF. 3).
 SQ SEQUENCE 235 AA; 27582 MW; 973ABDE8C7DE3D5 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 SRSRGH 161
 Db |||||
 63 SRSRGH 68
 RESULT 50
 ID UBL1 YEAST STANDARD; PRT; 236 AA.
 AC P35127;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ubiquitin carboxyl-terminal hydrolase YUHI (EC 3.4.19.12) (Ubiquitin
 DE thiolesterase).
 DE GN YUHI OR YJUR099W OR J1941.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes;
 OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
 ON NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miller H.I., Henzel W.J., Ridgway J.B., Kuang W.-J., Chisholm V.,
 RA Liu C.-C.;
 RT "Cloning and expression of a yeast ubiquitin-protein cleaving activity
 RT in Escherichia coli";
 RL Biotechnology 7:698-704(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ramezani Rad M., Kirchthath L., Hollenberg C.P.;
 RA Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Ubiquitin-protein hydrolase is involved both in the
 CC processing of ubiquitin precursors and of ubiquitinated proteins.
 CC This enzyme is a thiol protease that recognize and hydrolyze
 CC a peptide bond at the C-terminal glycine of ubiquitin.
 CC -1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
 CC ubiquitin + a thiol.
 CC -1- SIMILARITY: Belongs to peptidase family C12.
 CC -----
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 CC -----
 DR EMBL; Z49599; CAA89629.1; -.
 DR PIR; S51332; S51332.
 DR PDB; 1CMX; 27-JUL-99.
 DR Geronline; 141932; -.
 DR MEROPS; C12.002; -.
 DR SGD; S0003860; YUHI.
 DR GO; GO:0005737; C:cytoplasm; IC.
 DR InterPro; IPR001578; Peptidase C12.
 DR Pfam; PF01088; Peptidase C12; 1.
 DR PRINTS; PR00707; UECTHYDLASE.
 DR ProDom; PD350662; UCH_1; 1.
 DR PROSITE; PS00140; UCH_1; 1.
 DR KX Ub1 conjugation pathway; Hydrolase; Thiol protease; 3D-structure.
 FT ACT SITE 90 90 BY SIMILARITY.
 FT ACT SITE 166 166 BY SIMILARITY.
 FT ACT SITE 181 181 BY SIMILARITY.
 FT DOMAIN 43 60 UBIQUITIN BINDING 1 (POTENTIAL).
 FT DOMAIN 175 183 UBIQUITIN BINDING 2 (POTENTIAL).
 SQ SEQUENCE 236 AA; 26385 MW; D239FEE25798B395 CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GGIFEL 250
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Db 175 GGIFEL 180
RESULT 51
F801 SCHMA STANDARD; PRT; 238 AA.
AC P16463;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Female specific 800 protein (FS800).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=89181810; PubMed=2927441;
RA Reis M.G., Kuhn J., Blanton R., Davis A.H.;
RT "Localization and pattern of expression of a female specific mRNA in
Schistosoma mansoni.";
RL Mol. Biochem. Parasitol. 32:113-119(1989).
CC -1- FUNCTION: FS800 is likely to have some function in the production
or maintenance of the schistosome egg.
CC -1- DEVELOPMENTAL STAGE: Highest level only in mature worms, i.e.,
during egg production.
CC -1- MISCELLANEOUS: The two F800 proteins are read from two
overlapping reading frames.
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CC -----
DR EMBL; J03999; AAA29883.1; -.
FT DOMAIN 42 45 POLY-ASN.
FT DOMAIN 72 77 POLY-ASP.
SQ SEQUENCE 238 AA; 27993 MW; FDFC8E9F4181B7F1 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TRGRSN 134
Db 139 TRGRSN 144
|||||
DE Unknown thylakoid lumen protein, chloroplast precursor.
GN AT1G76450 OR F14G6.5 OR F15M4.5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Dunn P., Egtun P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
Mittscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.I.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

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RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana";
 RL Nature 408:816-820(2000).
 RP [2]
 RN SEQUENCE OF 81-89; 118-145; 166-181; 185-200 AND 218-236.
 RA Schubert M., Peterson U., Haas B., Funk C., Schroeder W.P.,
 RA Kieselbach T.;
 RT "The chloroplast lumen of Arabidopsis thaliana is a functionally
 RT important compartment";
 RL Submitted (AUG-2001) to Swiss-Prot.
 CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
 CC -!- CAUTION: Ref.1 sequences differ from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC -----
 DR EMBL; AC015450; AAG51945.1; ALT SEQ.
 DR EMBL; AC012394; AAF16656.1; ALT SEQ.
 KW Chloroplast; Thylakoid; Transit peptide.
 FT TRANSIT 1 26 CHLOROPLAST (POTENTIAL).
 FT TRANSIT 27 80 THYLAKOID.
 FT CHAIN 81 247 UNKNOWN THYLAKOID LUMEN PROTEIN.
 SQ SEQUENCE 247 AA; 27490 MW; FP2DB5627C7CEE67 CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 179 KGFYII 184
 Db 184 KGFYII 189
 RESULT 54
 PSE3_HUMAN
 ID PSE3_HUMAN STANDARD; PRT; 254 AA.
 AC Q12920; O35563; P97373; Q13172; Q9BQD9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Proteasome activator complex subunit 3 (Proteasome activator 28-gamma
 DE subunit) (PA28gamma) (PA28g) (Activator of multicatalytic protease
 DE subunit 3) (11S regulator complex gamma subunit) (REG-gamma) (Ki
 DE nuclear autoantigen).
 GN PSME3.
 OS Homo sapiens (Human), and
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606, 10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 EX MEDLINE=90183093; PubMed=1968796;
 RA Nikiido T., Shimada K., Shibata M., Hata M., Sakamoto M., Takasaki Y.,
 RA Sato C., Takahashi T., Nishida Y.;
 RT "Cloning and nucleotide sequence of cDNA for Ki antigen, a highly
 RT conserved nuclear protein detected with sera from patients with
 RT systemic lupus erythematosus";
 RL Clin. Exp. Immunol. 79:209-214(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC SPECIES=Human; TISSUE=B-cell, and Fetal brain;
 RX MEDLINE=95038831; PubMed=7951316;
 RA Albertsen H.M., Smith S.A., Mazoyer S., Fujimoto E., Stevens J.,

RA Williams B., Rodriguez P., Cropp C.S., Slijepcevic P., Carlson M.,
 RA Robertson M., Bradley P., Lawrence E., Harrington T., Sheng Z.M.,
 RA Hoopes R., Sternberg N., Brothman A., Callahan R., Ponder B.A.J.,
 RA White R.;
 RT "A physical map and candidate genes in the BRCA1 region on chromosome
 RT 17q12-21";
 RL Nat. Genet. 7:472-479(1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC SPECIES=Human; TISSUE=lung, Ovary, and Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
 RA Whiting M., Maman A., Young A.C., Shevchenko I., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE=97364691; PubMed=9218537;
 RA Kandil E., Kohda K., Ishibashi T., Tanaka K., Kasahara M.;
 RT "PA28 subunits of the mouse proteasome: primary structures and
 RT chromosomal localization of the genes";
 RL Immunogenetics 46:337-344(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Mouse; STRAIN=B10.BR;
 RX MEDLINE=97306277; PubMed=9162094;
 RA Jiang H., Monaco J.J.;
 RT "Sequence and expression of mouse proteasome activator PA28 and the
 RT related autoantigen Ki";
 RL Immunogenetics 46:93-98(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Mouse; STRAIN=129/SvJ;
 RX MEDLINE=98250122; PubMed=9590240;
 RA Kohda K., Ishibashi T., Shimbara N., Tanaka K., Matsuda Y.,
 RA Kasahara M.;
 RT "Characterization of the mouse PA28 activator complex gene family:
 RT complete organizations of the three member genes and a physical map of
 RT the approximately 150-kb region containing the alpha- and beta-subunit
 RT genes";
 RL J. Immunol. 160:4923-4935(1998).
 RN [7]
 RP SEQUENCE OF 82-135 FROM N.A.
 RC SPECIES=Human; TISSUE=Ovary;
 RX MEDLINE=95025896; PubMed=7545954;
 RA Miki Y., Swensen J., Shattuck-Eidens D., Futreal P.A., Harshman K.,
 RA Tavtigian S., Liu Q., Cochran C., Bennett L.M., Ding W.;
 RT "A strong candidate for the breast and ovarian cancer susceptibility
 RT gene BRCA1";
 RL Science 266:66-71(1994).
 CC -!- FUNCTION: Implicated in immunoproteasome assembly and required for
 CC efficient antigen processing. The PA28 activator complex enhances
 CC the generation of class I binding peptides by altering the
 CC cleavage pattern of the proteasome.
 CC -!- SUBUNIT: Homohexamers.
 CC -!- ALTERNATIVE PRODUCTS:


```

SEQUENCE FROM N.A.
RX MEDLINE=22426901; PubMed=12522265;
RA Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
RA Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J., A.,
RA Tananes J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.,
RT "Reductive genome evolution in Buchnera aphidicola.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
CC -!- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE
CC FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)
CC MOUNTED ON A CENTRAL ROD. THE ROD CONSISTS OF ABOUT 26 SUBUNITS OF
CC FLGG IN THE DISTAL PORTION, AND FLGB, FLGC AND FLGF ARE THOUGHT TO
CC BUILD UP THE PROXIMAL PORTION OF THE ROD WITH ABOUT 6 SUBUNITS
CC EACH (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to the flagella basal body rod proteins
CC family.
CC
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CC
DR EMBL; AB014017; AAC27035.1; -.
DR InterPro; IPR001444; Flag_bb_rod.
DR Pfam; PF00460; flg_bb_rod; 1.
DR PROSITE; PS00588; FLAGELLA_BB_ROD; 1.
KW Flagellum; Complete proteome.
SQ SEQUENCE 260 AA; 28215 MW; 089E1146CAD4690B CRC64;

Query Match 2.1%; Score 6; DB 1; Length 260;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 SEETIS 101
Db 57 SEETIS 62

RESULT 57
RL1_HSV2H
ID RL1_HSV2H STANDARD; PRT; 261 AA.
AC P28283;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Neurovirulence factor (ICP34.5).
GN RL1.
OS Herpes simplex virus (type 2 / strain H52).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10315;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92113549; PubMed=1662697;
RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
RT "Comparative sequence analysis of the long repeat regions and
RT adjoining parts of the long unique regions in the genomes of herpes
RT simplex viruses types 1 and 2.";
RL J. Gen. Virol. 72:3057-3075(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Dolan A.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC
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CC EMBL; D10471; BAA23428.1; -.
DR EMBL; Z86099; CAB06759.1; -.
DR EMBL; Z86099; CAB06706.1; -.
DR FIR; JQ1502; WMBEXE.
KW Repeat.
FT DOMAIN 3 12 2 X 5 AA TANDEM REPEATS OF R-R-R-G-P.
FT REPEAT 3 7
FT REPEAT 8 12 2 X 8 AA TANDEM REPEATS OF P-R-P-G-A-P-A-
FT DOMAIN 16 31 V.
FT REPEAT 16 23
FT REPEAT 24 31
SQ SEQUENCE 261 AA; 27908 MW; 4BBD13AF3D906D71 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 261;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 ERGPQR 121
Db 121 ERGPQR 126

RESULT 58
TNF5_AOTTR
ID TNF5_AOTTR STANDARD; PRT; 261 AA.
AC Q9BDM3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
DE L) (CD154 protein).
GN TNFSF5 OR CD40LG OR CD40L.
OS Aotus trivirgatus (Night monkey) (Douroucoulis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as Ige
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF344860; AA37542.1; -.
DR HSP; P29965; ITALY.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0005174; F:CD40 receptor binding; ISS.
DR GO; GO:0042100; P:B-cell proliferation; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.

```

DR GO: GO:0030168; P:Platelet activation; ISS.
 DR InterPro; IPR003263; TNF 5.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01702; CD40LIGAND.
 DR ProDom; PD008600; TNF 5; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF 1; 1.
 DR PROSITE; PS00049; TNF 2; 1.
 DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 261
 FT CHAIN 113 261
 FT DOMAIN 1 22
 FT TRANSMEM 23 43
 FT DOMAIN 44 261
 FT SITE 112 113
 FT DISULFID 178 218
 FT CARBOHYD 240 240
 SQ SEQUENCE 261 AA; 29357 MW; 85E1588B507901B5 CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 GGIFEL 250
 Db 226 GGIFEL 231
 RESULT 59
 TNF5_BOVIN STANDARD; PRT; 261 AA.
 AC P51749;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-related activation protein) (TRAP) (T cell antigen GP39).
 GN TNFSF5 OR CD40LG OR CD40L.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=9606582; PubMed=7590981;
 RA Mertens B.E.L.C.; Muriuki M.; Gaidulis L.;
 RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand and tumor necrosis factor alpha."
 RL Immunogenetics 42:430-431(1995).
 CC -1- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IGE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).
 CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC -----
 CC EMBL; Z48469; CA88363.1; -.
 CC PIR; S53090; S53090.
 CC HSP; P29965; 1ALY.
 CC GO: GO:0016021; C:integral to membrane; ISS.
 CC GO: GO:0005174; F:CD40 receptor binding; ISS.
 CC GO: GO:0042100; P:B-cell proliferation; ISS.
 CC GO: GO:0006954; P:inflammatory response; ISS.
 CC GO: GO:0007159; P:leukocyte cell adhesion; ISS.
 CC GO: GO:0030168; P:platelet activation; ISS.
 DR InterPro; IPR003263; TNF 5.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF_like.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01702; CD40LIGAND.
 DR ProDom; PD008600; TNF 5; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF 1; 1.
 DR PROSITE; PS00049; TNF 2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 261
 FT CHAIN 113 261
 FT DOMAIN 1 22
 FT TRANSMEM 23 46
 FT DOMAIN 47 261
 FT SITE 112 113
 FT DISULFID 178 218
 FT CARBOHYD 240 240
 SQ SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787FD CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 180 GFYIY 185
 Db 167 GFYIY 172
 RESULT 60
 TNF5_CALJA STANDARD; PRT; 261 AA.
 ID TNF5_CALJA
 AC Q9BDN3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (CD154 protein).
 GN TNFSF5 OR CD40LG OR CD40L.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F.; Bostik P.; Mayne A.E.; King C.L.; Genain C.P.; Weiss W.R.; Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."
 RL Immunogenetics 53:315-328(2001).
 CC -1- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IGE

```

CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC EMBL; AF344844; AAK37603.1; -.
CC HSP; P29965; IALY.
CC GO; GO:0016021; C: integral to membrane; ISS.
CC GO; GO:0005174; F: CD40 receptor binding; ISS.
CC GO; GO:0042100; P: B-cell proliferation; ISS.
CC GO; GO:0006954; P: inflammatory response; ISS.
CC GO; GO:0007159; P: leukocyte cell adhesion; ISS.
CC GO; GO:0030168; P: platelet activation; ISS.
CC InterPro; IPR003263; TNF 5.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01702; CD40LIGAND.
CC ProDom; PD008600; TNF 5; 1.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS50049; TNF 2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 261
FT CHAIN 113 261
FT DOMAIN 1 22
FT TRANSMEM 23 43
FT CHAIN 44 261
FT SITE 112 113
FT DISULFID 178 218
FT CARBOHYD 240 240
FT SEQUENCE 261 AA; 29360 MW; 10CA58BD923754EB CRC64;
Query Match 2.1%; Score 6; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GGFEL 250
DB 226 GGFEL 231
RESULT 61
XNLA CLOSA
AC P17137;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
DE xylan xylanohydrolase).
GN XNLA.
OS Clostridium saccharobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC NCBI_TaxID=169679;

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RN SEQUENCE FROM N.A.
RP STRAIN=P262;
RX MEDLINE=90245673; PubMed=2336398;
RA Zappe H., Jones W.A., Woods D.R.;
RT "Nucleotide sequence of a Clostridium acetobutylicum P262 xylanase
RT gene (xynB).";
RL Nucleic Acids Res. 18:2179-2179(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloridic
CC linkages in xyans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -!- CAUTION: Was originally thought to originate from
CC C.acetobutylicum.
CC
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CC
CC EMBL; M31726; AAA23287.1; -.
CC HSP; P36217; LXVO.
CC InterPro; IPR008985; ConA like lec gl.
CC InterPro; IPR001137; Glyco_hydro_11.
CC Pfam; PF00457; Glyco_hydro_11; 1.
CC PRINTS; PR00911; GLYDRLASE11.
CC PROSITE; PS00776; GLYCOSYL HYDROL F11 1; 1.
CC PROSITE; PS00777; GLYCOSYL HYDROL F11 2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 28
FT CHAIN 29 261
FT ACT SITE 152 152
FT ACT SITE 242 242
FT SEQUENCE 261 AA; 29032 MW; 339C3616F6D14AE CRC64;
Query Match 2.1%; Score 6; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 VIFTVL 25
DB 6 VIFTVL 11
RESULT 62
CTE2 HUMAN
AC Q8N6M3; Q9H3Y1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein C20orf142 precursor.
GN C20ORF142.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blake S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

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RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharalaino M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McClay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showlken R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulten J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20";
 RL Nature 414:865-871 (2001).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Udutin T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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 CC -----
 CC EMBL; AL117382; CAC04189.1; ALT_INIT.
 CC EMBL; BC029662; AAH29662.1;
 CC Genew; HGNC:16135; C20orf142.
 KW Signal; Transmembrane.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 262 PROTEIN C20ORF142.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 94 114 POTENTIAL.
 FT TRANSMEM 146 166 POTENTIAL.
 FT TRANSMEM 191 211 POTENTIAL.
 FT TRANSMEM 220 240 POTENTIAL.
 SQ SEQUENCE 262 AA; 29855 MW; 3822E7CFB6CDEB CRC64;

Query Match 2.1%; Score 6; DB 1; Length 262;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 159 SGHSFL 164
 Db 153 SGHSFL 158
 |||||

RESULT 63
 CTE2_MOUSE
 ID CTE2_MOUSE STANDARD; PRT; 262 AA.
 AC P59266;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein C20orf142 homolog precursor.
 GN C20ORF142.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta, Cerebellum, and Vein;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H.A., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs".
 RL Nature 420:563-573 (2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- CAUTION: Ref.1 (BAC29663) sequence differs from that shown due to
 CC a frameshift in position 192.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AK036997; BAC29663.1; ALT_FRAME.
 CC EMBL; AK040900; BAC30737.1; -.
 CC EMBL; AK043244; BAC31503.1; -.
 CC MGD; MGI:2444508; D930001I22Rik.
 KW Signal; Transmembrane.
 FT SIGNAL 1 39 POTENTIAL.
 FT CHAIN 40 262 PROTEIN C20ORF142 HOMOLOG.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 94 114 POTENTIAL.
 FT TRANSMEM 146 166 POTENTIAL.
 FT TRANSMEM 191 211 POTENTIAL.
 FT TRANSMEM 220 240 POTENTIAL.
 FT CONFLICT 169 169 E -> Q (IN REF. 1; BAC29663).
 FT CONFLICT 245 245 G -> P (IN REF. 1; BAC29663).

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SQ SEQUENCE 262 AA; 30016 MW; D28B971C521953BC CRC64;
Query Match      2.1%; Score 6; DB 1; Length 262;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 159 SGHSFL 164
    |||||
Db 153 SGHSFL 158

RESULT 64
YA23 METJA
ID YA23 METJA STANDARD; PRT; 262 AA.
AC Q58429;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Hypothetical ABC transporter ATP-binding protein MJ1023.
GN MJ1023.
OS Methanococcus jamaaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jamaaschii.";
RL Science 273:1058-1073 (1996).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U67545; AA899027.1; -.
DR F1R; F64427; F64427.
DR TIGR; MJ1023; -.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran_1
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC TRANSPORTER 1; 1.
DR PROSITE; PS00893; ABC TRANSPORTER 2; 1.
KW Hypothetical protein; ATP-binding; Transpporter; Complete proteome.
FT NP BIND 37 44 ATP (POTENTIAL).
SQ SEQUENCE 262 AA; 30316 MW; B195338E6CED777 CRC64;

Query Match      2.1%; Score 6; DB 1; Length 262;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 IPELKE 252
    |||||
Db 166 IPELKE 171

RESULT 65
YA23 METJA
ID YA23 METJA STANDARD; PRT; 262 AA.
AC Q58429;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Hypothetical ABC transporter ATP-binding protein MJ1023.
GN MJ1023.
OS Methanococcus jamaaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jamaaschii.";
RL Science 273:1058-1073 (1996).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
CC
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CC
CC EMBL; U67545; AA899027.1; -.
DR F1R; F64427; F64427.
DR TIGR; MJ1023; -.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran_1
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC TRANSPORTER 1; 1.
DR PROSITE; PS00893; ABC TRANSPORTER 2; 1.
KW Hypothetical protein; ATP-binding; Transpporter; Complete proteome.
FT NP BIND 37 44 ATP (POTENTIAL).
SQ SEQUENCE 262 AA; 30316 MW; B195338E6CED777 CRC64;

Query Match      2.1%; Score 6; DB 1; Length 262;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 164 LSNIHL 169
    |||||
Db 152 LSNIHL 157

RESULT 66
TNF5 CHICK
ID TNF5 CHICK STANDARD; PRT; 272 AA.
AC Q918D8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 15-MAR-2004 (Rel. 43; Last sequence update)
DT 15-MAR-2004 (Rel. 43; Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
DE L) (CD154 protein).
GN TNFSF5 OR CD40LG OR CD40L.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Spleen;
RA Tregaskes C.A., Young J.R., Burnside J.;
RT "Cloning of a putative chicken CD40 ligand.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as IGE
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
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EMBL; AF250958; AAC33972.1; -
 HSP; P27251.1; 2DEF
 InterPro; IPR000181; Pep_deformylase.
 Pfam; PF01327; Pep_deformylase; 1.
 PRINTS; PR01576; PDEFORMLASE.
 ProDom; PD003844; Pep_deformylase; 1.
 TIGRFAMs; TIGR00079; Pept_deformyl; 1.
 Protein biosynthesis; Hydrolase; Iron; Chloroplast; Transit peptide.
 TRANSIT 1
 CHAIN ? 273 CHLOROPLAST (POTENTIAL).
 PEPTIDE DEFORMYLASE.
 FT METAL 177 177 IRON (BY SIMILARITY).
 FT ACT SITE 214 214 BY SIMILARITY.
 FT METAL 171 171 IRON (BY SIMILARITY).
 FT METAL 213 213 IRON (BY SIMILARITY).
 FT METAL 217 217 IRON (BY SIMILARITY).
 FT CONFLICT 48 48 T -> N (IN REF. 4).
 FT CONFLICT 205 205 R -> S (IN REF. 1).
 SQ SEQUENCE 273 AA; 30610 MW; 25CDA90ED6D9603E CRC64;

Query Match 2.1%; Score 6; DB 1; Length 273;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 YPDPIL 221
 Db 86 YPDPIL 91

RESULT 68

DEFCLYCSES
 ID DEFCLYCSES STANDARD; PRT; 279 AA.
 AC Q9FV54;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Peptide deformylase, chloroplast precursor (EC 3.5.1.88) (PDF)
 DE (Polypeptide deformylase).
 GN PF1B.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20514156; PubMed=11060042;
 RA Giglione C., Serero A., Pierre M., Boisson B., Meinel T.;
 RT "Identification of eukaryotic peptide deformylases reveals
 universality of N-terminal protein processing mechanisms.";
 RL EMBO J. 19:5916-5929(2000).
 CC -!- FUNCTION: Removes the formyl group from the N-terminal Met of
 newly synthesized proteins (By similarity).
 CC -!- CATALYTIC ACTIVITY: Formyl-L-methionyl peptide + H(2)O = formate +
 methionyl peptide.
 CC -!- COFACTOR: Binds 1 iron(II) ion (By similarity).
 CC -!- SUBCELLULAR LOCATION: Chloroplast (Potential).
 CC -!- SIMILARITY: Belongs to the polypeptide deformylase family.
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 or send an email to license@isb-sib.ch).

CC EMBL; AF250958; AAC33972.1; -
 DR HSP; P27251.1; 2DEF
 DR InterPro; IPR000181; Pep_deformylase.
 DR Pfam; PF01327; Pep_deformylase; 1.
 DR PRINTS; PR01576; PDEFORMLASE.
 DR ProDom; PD003844; Pep_deformylase; 1.
 DR TIGRFAMs; TIGR00079; Pept_deformyl; 1.
 DR Protein biosynthesis; Hydrolase; Iron; Chloroplast; Transit peptide.
 FT TRANSIT 1
 CHAIN ? 279 PEPTIDE DEFORMYLASE.
 FT METAL 177 177 IRON (BY SIMILARITY).
 FT ACT SITE 214 214 BY SIMILARITY.
 FT METAL 220 220 IRON (BY SIMILARITY).
 FT METAL 223 223 IRON (BY SIMILARITY).
 SQ SEQUENCE 279 AA; 31197 MW; 750F6408FDAC4233 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 YPDPIL 221
 Db 92 YPDPIL 97

RESULT 69

KC2C ARATH
 ID KC2C ARATH STANDARD; PRT; 282 AA.
 AC P40229;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Casein kinase II beta' chain (CK II).
 GN CK2 OR AF4G17640 OR DL485W.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94339478; PubMed=8061317;
 RA Collinge M.A., Walker J.C.;
 RT "Isolation of an Arabidopsis thaliana casein kinase II beta subunit
 by complementation in Saccharomyces cerevisiae.";
 RL Plant Mol. Biol. 25:649-658(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98121113; PubMed=9461215;
 RA Bevan M., Bancroft I., Bent E., Love K., Goodman H.M., Dean C.,
 RA Bergkamp R., Dirkse W., van Staveren M., Striekema W., Drost L.,
 RA Ridley P., Hudson S.-A., Patel K., Murphy G., Piffanelli P.,
 RA Wedler H., Wambutt R., Weitzenger T., Pohl T., Terryn N.,
 RA Gielen J., Villarroel R., De Clercq R., van Montagu M., Lecharny A.,
 RA Aubourg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S.,
 RA Kotter P., Entian K.-D., Rieger M., Schaefer M., Funk B.,
 RA Mueller-Auer S., Silvey M., James R., Monfort A., Pons A.,
 RA Puigdomenech P., Douka A., Vouklatou E., Milioni D., Hatzopoulos P.,
 RA Piravandi E., Obermaier B., Hilbert H., Duesterhoef A., Moores T.,
 RA Jones J.D.G., Eberhart T., Palme K., Benes V., Rechmann S., Ansoorge W.,
 RA Cooke R., Berger C., Delsen M., Voet M., Volckaert G., Mewes H.-W.,
 RA Klosterman S., Schueller C., Chaltatzis N.;
 RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
 Arabidopsis thaliana".
 RL Nature 391:485-488(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoef A., Striekema W., Entian K.-D., Terryn N.,

RA Harris B., Anson W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang J.-J., Vandenbussche P.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenecker T., Bothe G., Ransperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirks W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berner S., Hempel S., Felbausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montegu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Wendlein A., Feilner R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedori F., Cooke R., Berger C., Monfort A., Casasuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Baquies M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielle C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Steneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courney J., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshua C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Macero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Grant S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:769-777(1999).
CC -1- FUNCTION: Plays a complex role in regulating the basal catalytic
CC activity of the alpha subunit (By similarity).
CC -1- SUBUNIT: Tetramer composed of an alpha chain, an alpha', one beta
CC chain and one beta' chain.
CC -1- PTM: Phosphorylated by alpha chain (By similarity).
CC -1- SIMILARITY: Belongs to the casein kinase 2 beta chain family.
CC
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CC
CC EMBL; U03984; AAA53234.1; --
CC EMBL; Z97343; CAB10544.1; --
CC EMBL; AL161546; CAB78767.1; --
CC PIR; S47968; S47968.
CC InterPro; IPR000704; CAS_kinase_II.
CC Pfam; PF01214; CK_II_beta; 1.
CC PRINTS; PR00472; CASNKINASEII.
CC ProDom; PD003829; CAS_kinase_II; 1.
CC PROSITE; PS01101; CK2_BETA; 1.
KW Transferase: Serine/threonine-protein kinase; Phosphorylation.
SQ SEQUENCE 282 AA; 31978 MW; 507EAB0A7415D1E6 CRC64;

Query Match

Best Local Similarity 2.4%; Score 6; DB 1; Length 282;

Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 155 ESRSG 160
Db 58 ESRSG 63
|||||
RESULT 70
DPHS SCHPO
ID DPHS SCHPO STANDARD; PRT; 283 AA.
AC 074838;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable diphthine synthase (EC 2.1.1.98) (Diphthamide biosynthesis
DE methyltransferase).
GN SPC576.14.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lynne R., Stewart A.,
RA Spouris J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Honesby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens S., Warren T.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer B., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Fumelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- FUNCTION: Required for the methylation step in diphthamide
CC biosynthesis.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 2-(3-carboxy-3-
CC aminopropyl)-L-histidine = S-adenosyl-L-homocysteine + 2-[3-
CC carboxy-3-(methylammonio)propyl]-L-histidine.
CC -1- PATHWAY: Diphthamide biosynthesis; second step.
CC -1- SIMILARITY: Belongs to the diphthine synthase family.
CC
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CC
CC EMBL; AL031798; CAA21193.1; --
CC PIR; T41424; T41424.
CC GeneDB SPombe; SPC576.14; --
CC InterPro; IPR000878; Cor/por_Metransf.
CC InterPro; IPR004551; Dphthm_synthase.
CC

```
DR Pfam; PF00590; TP methylase; 1.
DR TIGRfam; TIGR00522; dph5; 1.
DR KW Transferrase; Methyltransferase.
SQ SEQUENCE 283 AA; 32044 MW; FF3300910CECIAD7 CRC64;

Query Match      2.1%; Score 6; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 SLCVAV 33
DB 213 SLCVAV 218

RESULT 71
YNFH_ECOLI
ID YNFH_ECOLI STANDARD; PRT; 284 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Anaerobic dimethyl sulfoxide reductase chain ynfH (DMSO reductase
DE anchor subunit ynfH).
GN YNFH OR B1590.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayaashi K., Inada T., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Saeki G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377 (1996).
CC -!- FUNCTION: TERMINAL REDUCTASE DURING ANAEROBIC GROWTH ON
CC VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS. THE C SUBUNIT ANCHORS
CC THE OTHER TWO SUBUNITS TO THE MEMBRANE AND STABILIZES THE CATALYTIC
CC SUBUNITS (BY SIMILARITY).
CC -!- SUBUNIT: THE COMPLEX CONSIST OF THREE SUBUNITS: YNFF, THE
CC REDUCTASE, YNFG, AN ELECTRON TRANSFER PROTEIN, AND YNFH, A
CC MEMBRANE ANCHOR PROTEIN (Potential).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (By similarity).
CC -!- SIMILARITY: Strong, to E.coli dmsC.
CC
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CC
CC EMBL; AF000254; AAC74662.1; -
CC EMBL; D90801; BAA15314.1; ALT INIT.
CC EMBL; D90802; BAA15324.1; ALT_INIT.

PIR; H64914; H64914.
ECOGene; EG13846; ynfH.
DR InterPro; IPR007059; DmsC.
DR Pfam; PF04976; DmsC; 1.
KW Hypothetical protein; Oxidoreductase; Transmembrane; Inner membrane;
KW Complete proteome.
FT DOMAIN 1 9 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 10 30 POTENTIAL.
FT DOMAIN 31 45 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 46 66 POTENTIAL.
FT DOMAIN 67 86 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 87 107 POTENTIAL.
FT DOMAIN 108 115 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 116 136 POTENTIAL.
FT DOMAIN 137 148 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 149 169 POTENTIAL.
FT DOMAIN 170 180 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 181 201 POTENTIAL.
FT DOMAIN 202 222 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 223 243 POTENTIAL.
FT DOMAIN 244 250 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 251 271 POTENTIAL.
FT DOMAIN 272 284 PERIPLASMIC (POTENTIAL).
SQ SEQUENCE 284 AA; 30523 MW; 73F7D760FC4B1344 CRC64;

Query Match      2.1%; Score 6; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 VIFTVL 25
DB 11 VIFTVL 16

RESULT 72
LPXC_CHLVC
ID LPXC_CHLVC STANDARD; PRT; 285 AA.
AC Q824Q4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UDP-3-O-(3-hydroxymyristoyl) N-acetylglucosamine deacetylase
DE (EC 3.5.1.-) (UDP-3-O-acetyl-GlcNAc deacetylase).
GN LPXC OR CCA000088.
OS Chlamydomophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=833557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
RA Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
RA Fraser C.M.;
RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae."
RL Nucleic Acids Res. 31:2134-2147 (2003).
CC -!- FUNCTION: Involved in the biosynthesis of lipid A, a
CC phosphorylated glycolipid that anchors the lipopolysaccharide to
CC the outer membrane of the cell (By similarity).
CC -!- CATALYTIC ACTIVITY: UDP-3-O-(3-hydroxytetradecanoyl)-N-
CC acetylglucosamine + H(2)O = UDP-3-O-(3-hydroxytetradecanoyl)-
CC glucosamine + acetate.
CC -!- PATHWAY: Lipid A biosynthesis; second step.
CC -!- SIMILARITY: Belongs to the lpxC family.
CC
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CC -----

DR EMBL; AE016994; AAP04840.1; -
DR TIGR; CCA00088; -
DR HAMAP; MF 00388; -; 1.
DR InterPro; IPR004463; LpxC.
DR Pfam; PF03331; LpxC; 1.
DR TIGRFAMs; TIGR00325; lpxC; 1.
KW Hydrolase; Lipid A biosynthesis; Lipid synthesis; Complete proteome.
SQ SEQUENCE 285 AA; 31421 MW; 300EC1D08DB9403D9 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 285;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 ALGRKI 151
| | | | |
DB 274 ALGRKI 279

RESULT 73

YHCS_HAEIN
ID YHCS_HAEIN STANDARD; PRT; 288 AA.
AC P43011;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Putative HTH-type transcriptional regulator H11364 (ORF2).
GN H11364.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uitterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
CC
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CC -----

DR EMBL; U20964; AAC43726.1; -
DR EMBL; U32816; AAC23011.1; -
DR FPR; D64171; D64171.
DR TIGR; H11364; -.

DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS0931; HTH_LysR; 1.
KW Hypothetical protein; Transcription regulation; DNA-binding;
KW Complete proteome.
FT DOMAIN 1 59 HTH_LysR-TYPE
FT DNA_BIND 19 38 H-T-H MOTIF (POTENTIAL).
FT CONFLICT 281 288 VTGSLNLF -> RAFTFLSGGLGCLSEIWNHEDNI
FT (IN REF. 1).
SQ SEQUENCE 288 AA; 32422 MW; EEF3C22374352980 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 KQONIS 111
| | | | |
DB 24 KQONIS 29

RESULT 74

EGCI_LISIN
ID EGCI_LISIN STANDARD; PRT; 291 AA.
AC Q92A19;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable GTPase engC protein 1 (EC 3.6.1.-).
GN ENGCI OR LIN1933.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krest J., Kuhn M., Kunst F., Kurapkut G.,
RA Madsen E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordieck G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RL "Comparative genomics of Listeria species.";
Science 294:849-852(2001)
CC -!- FUNCTION: Unusual circularly permuted GTPase that catalyzes rapid
CC hydrolysis of GTP with a slow catalytic turnover (By similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SIMILARITY: Contains 1 engC GTPase domain.
CC
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CC -----

DR EMBL; AL596170; CAC97163.1; -
DR PIR; AC1674; AC1674.
DR ListLiast; LIN01933; -
DR HAMAP; MF 01820; -; 1.
DR InterPro; IPR004881; DUF258.
DR Pfam; PF03193; DUF258; 1.
DR TIGRFAMs; TIGR00157; TIGR00157; 1.
DR PROSITE; PS0936; ENG_C GTPASE; 1.
KW Hydrolase; GTP-binding; Complete proteome.

FT DOMAIN 72 219 ENG C GTPASE.
FT NP_BIND 112 115 GTP (PROBABLE).
FT NP_BIND 164 171 GTP (PROBABLE).
FT NP_BIND 214 218 GTP (PROBABLE).
FT SITE 245 258 KNUCKLE-LIKE CYSTEINE CLUSTER.
SQ SEQUENCE 291 AA; 32741 MW; 2C489FBBFDD69A61 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 NISPLV 114
Db 35 NISPLV 40

RESULT 75

EGCI_LISMO
ID EGCI_LISMO STANDARD; PRT; 291 AA.
AC Q8Y680;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable GTPase engC protein 1 (EC 3.6.1.-).
GN EGCI OR LMO1819.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Gautier K.-D., Pshi H., Garcia-del Portillo F., Garrido P.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RL "Comparative genomics of Listeria species.";
Science 294:849-852(2001).
CC -!- FUNCTION: Unusual circularly permuted GTPase that catalyzes rapid
CC hydrolysis of GTP with a slow catalytic turnover (By similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SIMILARITY: Contains 1 engC GTPase domain.

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DR EMBL; AL591981; CAC99897.1; -.
DR PIR; AC1302; AC1302.
DR ListList; LMO01819; -.
DR HAMAP; MF_01820; -; 1.
DR InterPro; IPR004881; DUF258.
DR Pfam; PF03193; DUF258; 1.
DR TIGRFAMs; TIGR00157; TIGR00157; 1.
DR PROSITE; PS50936; ENG C GTPASE; 1.
KW Hydrolase; GTP-binding; Complete proteome.
FT DOMAIN 72 219 ENG C GTPASE.
FT NP_BIND 112 115 GTP (PROBABLE).
FT NP_BIND 164 171 GTP (PROBABLE).
FT NP_BIND 214 218 GTP (PROBABLE).
FT SITE 245 258 KNUCKLE-LIKE CYSTEINE CLUSTER.
SQ SEQUENCE 291 AA; 32744 MW; 4C44B33EE7159B56 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 NISPLV 114
Db 35 NISPLV 40

Search completed: March 23, 2004, 09:22:44
Job time : 23 secs

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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:21:00 ; Search time 22 seconds
(without alignments)

659.404 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MAMMEVQGPSLQGTCLIV.....NEHLIDMDHEASFFGFLVG 281

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/pCTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	281	100.0	281	1	US-08-670-354-2
2	281	100.0	281	3	US-08-584-031-1
3	281	100.0	281	3	US-08-780-496-1
4	281	100.0	281	3	US-08-883-086-10
5	281	100.0	281	3	US-09-320-424-2
6	281	100.0	281	4	US-09-333-593A-6
7	281	100.0	281	4	US-09-157-864-11
8	281	100.0	281	4	US-09-825-563-2
9	281	100.0	281	4	US-10-039-785-66
10	281	100.0	281	5	PCT-US96-10895-2
11	279	99.3	279	4	US-09-072-993C-3
12	187	66.5	253	3	US-09-320-424-11
13	187	66.5	253	4	US-09-825-563-11
14	187	66.5	256	3	US-09-320-424-13
15	187	66.5	256	4	US-09-825-563-13
16	174	61.9	177	3	US-09-105-343A-7
17	161	57.3	161	4	US-09-565-423-7
18	90	32.0	101	1	US-08-670-354-4
19	90	32.0	101	3	US-09-320-424-4
20	90	32.0	101	4	US-09-825-563-4
21	90	32.0	101	5	PCT-US96-10895-4
22	85	30.2	85	4	US-09-632-287A-12
23	24	8.5	59	4	US-09-621-976-6479
24	15	5.3	15	4	US-09-628-665-14
25	15	5.3	19	4	US-09-628-665-32
26	14	5.0	183	3	US-09-105-343A-8
27	14	5.0	291	1	US-08-670-354-6

28	14	5.0	291	3	US-09-320-424-6	Sequence 6, Appli
29	14	5.0	291	4	US-09-825-563-6	Sequence 6, Appli
30	14	5.0	291	5	PCT-US96-10895-6	Sequence 6, Appli
31	12	4.3	87	4	US-09-632-287A-13	Sequence 13, Appli
32	7	2.5	96	1	US-07-972-481-2	Sequence 2, Appli
33	33	2.5	172	4	US-09-134-001C-5649	Sequence 5649, Ap
34	7	2.5	209	4	US-09-096-724B-8	Sequence 8, Appli
35	7	2.5	209	4	US-09-096-724B-24	Sequence 24, Appli
36	7	2.5	274	4	US-09-489-039A-7595	Sequence 7595, Ap
37	7	2.5	429	4	US-09-198-452A-189	Sequence 189, App
38	7	2.5	554	4	US-08-909-125-6	Sequence 6, Appli
39	7	2.5	700	4	US-09-851-642-34	Sequence 34, Appli
40	7	2.5	2071	3	US-09-415-522-6	Sequence 6, Appli
41	6	2.1	6	4	US-09-628-665-13	Sequence 13, Appli
42	6	2.1	10	4	US-09-628-665-31	Sequence 31, Appli
43	6	2.1	24	4	US-09-612-402B-26	Sequence 26, Appli
44	6	2.1	28	4	US-09-030-619-50	Sequence 50, Appli
45	6	2.1	46	4	US-08-858-207A-268	Sequence 268, App
46	6	2.1	62	4	US-09-328-352-6548	Sequence 6548, Ap
47	6	2.1	78	4	US-09-107-532A-5502	Sequence 5502, Ap
48	6	2.1	83	4	US-09-543-681A-5440	Sequence 5440, Ap
49	6	2.1	87	4	US-09-328-352-5745	Sequence 5745, Ap
50	6	2.1	104	3	US-08-946-329A-99	Sequence 99, Appli
51	6	2.1	105	4	US-09-543-681A-8267	Sequence 8267, Ap
52	6	2.1	106	2	US-08-822-830B-4	Sequence 4, Appli
53	6	2.1	106	2	US-08-950-660-4	Sequence 4, Appli
54	6	2.1	106	4	US-09-157-452B-4	Sequence 4, Appli
55	6	2.1	106	4	US-08-454-899G-10	Sequence 10, Appli
56	6	2.1	106	5	PCT-US93-00030-4	Sequence 4, Appli
57	6	2.1	106	5	PCT-US93-00924-4	Sequence 4, Appli
58	6	2.1	114	4	US-09-621-976-5264	Sequence 5264, Ap
59	6	2.1	116	4	US-09-134-001C-5132	Sequence 5132, Ap
60	6	2.1	117	4	US-09-489-039A-9835	Sequence 9835, Ap
61	6	2.1	119	4	US-08-635-886C-248	Sequence 248, App
62	6	2.1	119	4	US-08-974-690C-248	Sequence 248, App
63	6	2.1	128	4	US-08-635-886C-240	Sequence 240, App
64	6	2.1	128	4	US-08-974-690C-240	Sequence 240, App
65	6	2.1	129	4	US-09-134-000C-3666	Sequence 3666, Ap
66	6	2.1	134	4	US-09-252-991A-18565	Sequence 18565, A
67	6	2.1	135	4	US-09-252-991A-22722	Sequence 22722, A
68	6	2.1	135	4	US-09-252-991A-27904	Sequence 27904, A
69	6	2.1	137	4	US-09-328-352-4265	Sequence 4265, Ap
70	6	2.1	138	4	US-09-134-001C-3776	Sequence 3776, Ap
71	6	2.1	140	4	US-09-134-000C-6375	Sequence 6375, Ap
72	6	2.1	144	4	US-09-593-887-8	Sequence 8, Appli
73	6	2.1	145	4	US-09-134-001C-3901	Sequence 3901, Ap
74	6	2.1	147	4	US-09-461-325-458	Sequence 458, App
75	6	2.1	147	4	US-10-012-542-458	Sequence 458, App
76	6	2.1	149	3	US-08-836-075A-34	Sequence 34, Appli
77	6	2.1	149	3	US-08-836-075A-34	Sequence 40, Appli
78	6	2.1	149	4	US-08-635-886C-244	Sequence 244, App
79	6	2.1	149	4	US-08-635-886C-247	Sequence 247, App
80	6	2.1	149	4	US-08-974-690C-244	Sequence 244, App
81	6	2.1	149	4	US-08-974-690C-247	Sequence 247, App
82	6	2.1	152	4	US-09-252-991A-31484	Sequence 31484, A
83	6	2.1	155	2	US-08-984-172-3	Sequence 3, Appli
84	6	2.1	161	4	US-09-134-001C-3996	Sequence 3996, Ap
85	6	2.1	166	4	US-09-615-192A-273	Sequence 273, App
86	6	2.1	174	4	US-09-131-237C-2	Sequence 2, Appli
87	6	2.1	184	2	US-08-633-298-4	Sequence 4, Appli
88	6	2.1	185	4	US-09-328-352-7577	Sequence 7577, Ap
89	6	2.1	192	1	US-08-086-428B-93	Sequence 93, Appli
90	6	2.1	192	2	US-08-468-570-93	Sequence 93, Appli
91	6	2.1	192	2	US-08-290-665A-93	Sequence 93, Appli
92	6	2.1	192	4	US-08-466-601A-93	Sequence 93, Appli
93	6	2.1	192	5	PCT-US95-10398-93	Sequence 93, Appli
94	6	2.1	193	4	US-08-635-886C-212	Sequence 212, App
95	6	2.1	193	4	US-08-974-690C-212	Sequence 212, App
96	6	2.1	194	4	US-08-311-731A-273	Sequence 273, App
97	6	2.1	202	4	US-09-134-000C-3978	Sequence 3978, Ap
98	6	2.1	204	4	US-09-252-991A-31049	Sequence 31049, A
99	6	2.1	211	4	US-09-543-681A-8111	Sequence 8111, Ap
100	6	2.1	214	2	US-08-984-172-1	Sequence 1, Appli

ALIGNMENTS

```

RESULT 1
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

Query Match 100.0%; Score 281; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVVFTNELKQMDKYSKGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVVFTNELKQMDKYSKGIACFLKE 60
QY 61 DDSYNDPNDDESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQKNISPLVRRGPQ 120
DB 61 DDSYNDPNDDESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQKNISPLVRRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240

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QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

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RESULT 2

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US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

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Query Match 100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVVFTNELKQMDKYSKGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVVFTNELKQMDKYSKGIACFLKE 60
QY 61 DDSYNDPNDDESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQKNISPLVRRGPQ 120
DB 61 DDSYNDPNDDESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQKNISPLVRRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

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RESULT 3

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US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: Apo-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435

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; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5415
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-780-496-1

Query Match      100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-379;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVGGSPGLGTCVLIVFTVLLQSLCAVAVTVYFTNELKOMQDKYSKSGIACFLKE 60
Db      1 MAMMEVGGSPGLGTCVLIVFTVLLQSLCAVAVTVYFTNELKOMQDKYSKSGIACFLKE 60

QY      61 DSDYWDNDNDSESMNSPCQVQKWQLRQLVRKMLATSEETISTVQEKQONISPLVRERGPQ 120
Db      61 DSDYWDNDNDSESMNSPCQVQKWQLRQLVRKMLATSEETISTVQEKQONISPLVRERGPQ 120

QY      121 RVAAHITGTRSRNTLSPNSKNEKALGRKINSWESSRSGHSFTLNHLRNGELVVIHEKG 180
Db      121 RVAAHITGTRSRNTLSPNSKNEKALGRKINSWESSRSGHSFTLNHLRNGELVVIHEKG 180

QY      181 FYIYISQTYFRFQBEIKENTKNDQMVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
Db      181 FYIYISQTYFRFQBEIKENTKNDQMVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

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; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
US-08-883-086-10

Query Match 100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCTVLIIVFTLLQSLCAVTVYVFTNELKMQDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCTVLIIVFTLLQSLCAVTVYVFTNELKMQDKYSKSGIACFLKE 60

Qy 61 DDSVDPNDEESMNSPCQWKQRLVRKMIILRTSEETISTVQEKQONTSPLVRESGPQ 120
Db 61 DDSVDPNDEESMNSPCQWKQRLVRKMIILRTSEETISTVQEKQONTSPLVRESGPQ 120

Qy 121 RVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVVIHEKG 180
Db 121 RVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVVIHEKG 180

Qy 181 FYIYSQTYFRFOEIKENTKDKQWQVIYIKYTSYDPDPTLLMKSAENSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKDKQWQVIYIKYTSYDPDPTLLMKSAENSCWSKDAEYGLY 240

Qy 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

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RESULT 4
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883.086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:

QY 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIEHG 180
Db 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIEHG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 6

US-09-333-593A-6
; Sequence 6, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R. A.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-5008-2
; CURRENT APPLICATION NUMBER: US/09/333.593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 281
; TYPE: PRI
; ORGANISM: HOMO SAPIENS
US-09-333-593A-6

Query Match 100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIEHG 180
Db 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIEHG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7

US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L. 41,113
; REGISTRATION NUMBER: 6111.N CN1
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-157-864-11

Query Match 100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIEHG 180
Db 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIEHG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8

US-09-825-563-2
; Sequence 2, Application US/09825563
; Patent No. 6521228

```

; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-09-825-563--2

Query Match      100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAMMEVQGGPSLGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
      |||
Db      1  MAMMEVQGGPSLGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
      |||

QY      61  DDSYDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
      |||
Db      61  DDSYDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
      |||

QY      121  RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLGELVTHEKG 180
      |||
Db      121  RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLGELVTHEKG 180
      |||

QY      181  FYYIYSQTYRFOBEIKENTKNDKQWQVYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
      |||
Db      181  FYYIYSQTYRFOBEIKENTKNDKQWQVYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
      |||

QY      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
      |||
Db      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
      |||

RESULT 9
US-10-039-785-66
; Sequence 66, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09

Query Match      100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAMMEVQGGPSLGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
      |||
Db      1  MAMMEVQGGPSLGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
      |||

QY      61  DDSYDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
      |||
Db      61  DDSYDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
      |||

QY      121  RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLGELVTHEKG 180
      |||
Db      121  RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLGELVTHEKG 180
      |||

QY      181  FYYIYSQTYRFOBEIKENTKNDKQWQVYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
      |||
Db      181  FYYIYSQTYRFOBEIKENTKNDKQWQVYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
      |||

QY      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
      |||
Db      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
      |||

RESULT 10
PCT-US96-10895-2
; Sequence 2, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match          100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMEVQGGPSLGQTCVLIIVFTVLLQSLCVAIVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMEVQGGPSLGQTCVLIIVFTVLLQSLCVAIVYVFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYNDPDEESMNSPCWQVKWQLRQVLRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DSDYNDPDEESMNSPCWQVKWQLRQVLRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDILLMKSARNCSWCKDAEYGLYI 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDILLMKSARNCSWCKDAEYGLYI 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 11
US-09-072-993C-3
; Sequence 3, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-3

Query Match          99.3%; Score 279; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 6.2e-277;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVQGGPSLGQTCVLIIVFTVLLQSLCVAIVYVFTNELKQMDKYSGIACFLKEDD 62
Db 1 MMEVQGGPSLGQTCVLIIVFTVLLQSLCVAIVYVFTNELKQMDKYSGIACFLKEDD 60

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QY 63 SYNDPDEESMNSPCWQVKWQLRQVLRKMLRTSEETISTVQEKQONISPLVRERGPO 122
Db 61 SYNDPDEESMNSPCWQVKWQLRQVLRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 123 AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGKGY 182
Db 121 AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGKGY 180
QY 183 YIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDILLMKSARNCSWCKDAEYGLYI 242
Db 181 YIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDILLMKSARNCSWCKDAEYGLYI 240
QY 243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279

RESULT 12
US-09-320-424-11
; Sequence 11, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-11

Query Match          66.5%; Score 187; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.5e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVRERGPOVAAHITGRGRSNTLSSPNSKNEKALGRKINSW 154
Db 67 TSEETISTVQEKQONISPLVRERGPOVAAHITGRGRSNTLSSPNSKNEKALGRKINSW 126
QY 155 ESSRSGHSFSLNHLRNGELVIEHGKGYIYSQTYFRFOEIKENTKNDKQMVQYIYKYT 214
Db 127 ESSRSGHSFSLNHLRNGELVIEHGKGYIYSQTYFRFOEIKENTKNDKQMVQYIYKYT 186
QY 215 SYDDPILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 187 SYDDPILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246
QY 275 FGAFLVG 281
Db 247 FGAFLVG 253

RESULT 13
US-09-825-563-11
; Sequence 11, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:

```

RESULT 14
US-09-320-424-13
; Sequence 13, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PR1

Db 250 FGAFLVG 256

RESULT 16

US-09-105-343A-7

; Sequence 7, Application US/09105343A

; Patent No. 6207642

; GENERAL INFORMATION:

; APPLICANT: WILEY, S.R.

; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL

; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Road

; CITY: Abbott Park

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-6050

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/105.343A

; FILING DATE: 12-FEB-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US98/02859

; FILING DATE: 12-FEB-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: BECKER, Cheryl L.

; REGISTRATION NUMBER: 35,441

; REFERENCE/DOCKET NUMBER: 6048.US.P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 847-935-1729

; TELEFAX: 847-938-2623

; TELEX:

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 177 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6207642e

US-09-105-343A-7

Query Match

Best Local Similarity 61.9%; Score 174; DB 3; Length 177;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 EKQONISPLVRGQPVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSL 164

Db 1 EKQONISPLVRGQPVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSL 60

QY 165 SNLHRLNGELVHEKGFYIYSQTFRQBEIKENTKDKQMVYIKYTSYPPDILLMK 224

Db 61 SNLHRLNGELVHEKGFYIYSQTFRQBEIKENTKDKQMVYIKYTSYPPDILLMK 120

QY 225 SARNSCWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Db 121 SARNSCWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 174

RESULT 17

US-09-565-423-7

; Sequence 7, Application US/09565423

; Patent No. 6475987

; GENERAL INFORMATION:

; APPLICANT: Shu, Hong-Bing

; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 2879-72

; CURRENT APPLICATION NUMBER: US/09/565,423

; CURRENT FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: UNKNOWN

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/132,892

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 161

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-565-423-7

Query Match

Best Local Similarity 57.3%; Score 161; DB 4; Length 161;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 180

Db 1 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 60

QY 181 FYIYSQTFRQBEIKENTKDKQMVYIKYTSYPPDILLMKSAKNSCWKDAEYGLY 240

Db 61 FYIYSQTFRQBEIKENTKDKQMVYIKYTSYPPDILLMKSAKNSCWKDAEYGLY 120

QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

Db 121 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 161

RESULT 18

US-08-670-354-4

; Sequence 4, Application US/08670354

; Patent No. 5763223

; GENERAL INFORMATION:

; APPLICANT: Steven R. Wiley and

; APPLICANT: Raymond G. Goodwin.

; TITLE OF INVENTION: Cytokine That Induces Apoptosis

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple 7.5.2

; SOFTWARE: Microsoft Word, Version 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/670,354

; FILING DATE: 25-JUN-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/496,632

; FILING DATE: 29-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/548,368

; FILING DATE: 01-NOV-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Anderson, Kathryn A.

; REGISTRATION NUMBER: 32,172

; REFERENCE/DOCKET NUMBER: 2835-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644

; TELEX: 756822


```
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 101 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-670-354-4

Query Match
Best Local Similarity 32.0%; Score 90; DB 1; Length 101;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90
Db 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90

RESULT 19
US-09-320-424-4
; Sequence 4, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
; US-09-320-424-4

Query Match
Best Local Similarity 32.0%; Score 90; DB 3; Length 101;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90
Db 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90

RESULT 20
US-09-825-563-4
; Sequence 4, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563

Query Match
Best Local Similarity 32.0%; Score 90; DB 3; Length 101;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90
Db 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90

RESULT 21
PCT-US96-10895-4
; Sequence 4, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822

Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90
Db 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90

RESULT 21
PCT-US96-10895-4
; Sequence 4, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
```

```
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 101 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; PCT-US96-10895-4

Query Match      32.0%; Score 90; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.1e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCLVLIFFTVLLQSLCVAVTVVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVLIFFTVLLQSLCVAVTVVFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYWDNDDESMNSPCWQVXWQLRQLVRK 90
Db 61 DDSYWDNDDESMNSPCWQVXWQLRQLVRK 90

RESULT 22
US-09-632-287A-12
; Sequence 12, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-632-287A-12

Query Match      30.2%; Score 85; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.4e-79;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 ERGPQVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHLRNGELV 175
Db 1 ERGPQVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHLRNGELV 60

Qy 176 IHEKGFYIYSQTYFRFQEEIKENT 200
Db 61 IHEKGFYIYSQTYFRFQEEIKENT 85

RESULT 23
US-09-621-976-6479
; Sequence 6479, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6479
; LENGTH: 59
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 27
; OTHER INFORMATION: Xaa = Glu,Gln
; NAME/KEY: UNSURE
; LOCATION: 34
; OTHER INFORMATION: Xaa = Glu,Val
; NAME/KEY: UNSURE
; LOCATION: 33,57
; OTHER INFORMATION: Xaa = Leu,Pro
; NAME/KEY: UNSURE
; LOCATION: 25,32
; OTHER INFORMATION: Xaa = Leu,Val
; OTHER INFORMATION: Xaa = Leu,Val
US-09-621-976-6479

Query Match      8.5%; Score 24; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCLVLIFFTV 24
Db 1 MAMMEVGGPSLGGTCLVLIFFTV 24

RESULT 24
US-09-628-665-14
; Sequence 14, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628,665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-14

Query Match      5.3%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 RFQBEIKENTKNDKQ 205
Db 1 RFQBEIKENTKNDKQ 15

RESULT 25
US-09-628-665-32
; Sequence 32, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628,665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771e1 Sequence
US-09-628-665-32

Query Match          5.3%; Score 15; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 RFQEEIKENTKNDKQ 205
Db 3 RFQEEIKENTKNDKQ 17

RESULT 26
US-09-105-343A-8
; Sequence 8, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-8

Query Match          5.0%; Score 14; DB 3; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 VQYIKYKTSYPDPI 220
Db 109 VQYIKYKTSYPDPI 122

RESULT 27
US-09-105-343A-8
; Sequence 8, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-8

Query Match          5.0%; Score 14; DB 3; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 VQYIKYKTSYPDPI 220
Db 109 VQYIKYKTSYPDPI 122

RESULT 28
US-09-320-424-6
; Sequence 6, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
```

```
US-08-670-354-6
; Sequence 6, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-6

Query Match          5.0%; Score 14; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 VQYIKYKTSYPDPI 220
Db 217 VQYIKYKTSYPDPI 230

RESULT 28
US-09-320-424-6
; Sequence 6, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
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; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 291
; TYPE: PRT
; ORGANISM: murine
US-09-320-424-6

Query Match 5.0%; Score 14; DB 3; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VOYIYKTSYDPPI 220
Db 217 VOYIYKTSYDPPI 230

RESULT 29
PCT-US96-10895-6
; Sequence 6, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 291
; TYPE: PRT
; ORGANISM: murine
US-09-825-563-6

Query Match 5.0%; Score 14; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VOYIYKTSYDPPI 220
Db 217 VOYIYKTSYDPPI 230

RESULT 30
PCT-US96-10895-6
; Sequence 6, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle

STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-6

Query Match 5.0%; Score 14; DB 5; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VOYIYKTSYDPPI 220
Db 217 VOYIYKTSYDPPI 230

RESULT 31
US-09-632-287A-13
; Sequence 13, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mouse
US-09-632-287A-13

Query Match 4.3%; Score 12; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 YIYQTYFRFQE 194
|||||

Db 65 YIYSQYRFQE 76

RESULT 32
US-07-972-481-2
; Sequence 2, Application US/07972481
; Patent No. 5578453
; GENERAL INFORMATION:
; APPLICANT: MCDONALD, PETER J
; APPLICANT: JOHNSON, ALAN M
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TOXOPLASMA ANTIGENS AND
; TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 GATEHOUSE ROAD
; CITY: FALLS CHURCH
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,481
; FILING DATE: 12-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: INTERNATIONAL PCT/AU91/00347
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 446-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-972-481-2

Query Match 2.5%; Score 7; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FQEEIKE 198
Db 2 FQEEIKE 8

RESULT 33
US-09-134-001C-5649
; Sequence 5649, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5649

; LENGTH: 172
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5649

Query Match 2.5%; Score 7; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ASFFGAF 278
Db 105 ASFFGAF 111

RESULT 34
US-09-096-724B-8
; Sequence 8, Application US/09096724B
; Patent No. 6548290
; GENERAL INFORMATION:
; APPLICANT: McGarry, Thomas J.
; APPLICANT: Kroll, Kristen
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Geminin Gene and Protein
; FILE REFERENCE: 0725.1055-001
; CURRENT APPLICATION NUMBER: US/09/096,724B
; CURRENT FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/085,371
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: human
US-09-096-724B-8

Query Match 2.5%; Score 7; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QBEIKEN 199
Db 9 QBEIKEN 15

RESULT 35
US-09-096-724B-24
; Sequence 24, Application US/09096724B
; Patent No. 6548290
; GENERAL INFORMATION:
; APPLICANT: McGarry, Thomas J.
; APPLICANT: Kroll, Kristen
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Geminin Gene and Protein
; FILE REFERENCE: 0725.1055-001
; CURRENT APPLICATION NUMBER: US/09/096,724B
; CURRENT FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/085,371
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 209
; TYPE: PRT
; ORGANISM: human
US-09-096-724B-24

Query Match 2.5%; Score 7; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QBEIKEN 199
Db 9 QBEIKEN 15

Db 9 QEEIKEN 15

RESULT 36

US-09-489-039A-7595
; Sequence 7595, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709-2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 7595

; LENGTH: 274

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-7595

Query Match

Best Local Similarity 2.5%; Score 7; DB 4; Length 274;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 ISPLVRE 116

Db 117 ISPLVRE 123

RESULT 37

US-09-198-452A-189

; Sequence 189, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 189

; LENGTH: 429

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-189

Query Match

Best Local Similarity 2.5%; Score 7; DB 4; Length 429;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSRGH 161

Db 248 ESSRSRGH 254

RESULT 38

US-08-909-125-6

; Sequence 6, Application US/08909125

; Patent No. 6495737

; GENERAL INFORMATION:

; APPLICANT: KLESSIG, DANIEL

; APPLICANT: GUO, AILAN

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMPROVING

; TITLE OF INVENTION: SALICYLIC ACID-INDEPENDENT SYSTEMIC ACQUIRED DISEASE RESISTANCE

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dann, Dorfman, Herrell and Skillman

; STREET: 1601 Market Street Suite 720

; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,125
; FILING DATE: 11-AUG-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,033
; FILING DATE: 12-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: JANET E. REED, PH.D.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-563-4100
; TELEFAX: 215-563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 554 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-909-125-6

Query Match

Best Local Similarity 2.5%; Score 7; DB 4; Length 554;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 KALGRKI 151

Db 477 KALGRKI 483

RESULT 39

US-09-831-642-34

; Sequence 34, Application US/09831642

; Patent No. 6635751

; GENERAL INFORMATION:

; APPLICANT: HAZE, Kyosuke et al.

; TITLE OF INVENTION: ENDOPLASMIC RETICULUM STRESS TRANSCRIPTION FACTORS ATF6 AND CREB

; FILE REFERENCE: 1422-0474P

; CURRENT APPLICATION NUMBER: US/09/831,642

; CURRENT FILING DATE: 2001-05-11

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 34

; LENGTH: 700

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-831-642-34

Query Match

Best Local Similarity 2.5%; Score 7; DB 4; Length 700;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TVLLQSL 29

Db 263 TVLLQSL 269

RESULT 40
US-09-415-522-6
; Sequence 6, Application US/09415522A
; Patent No. 6291660
; GENERAL INFORMATION:
; APPLICANT: Gaffney, Thomas
; APPLICANT: Wendland, Juergen
; APPLICANT: Philippsen, Peter
; TITLE OF INVENTION: No. 6291660el Fungal Genes Required For No. 6291660mal Growth And
; TITLE OF INVENTION: Development
; FILE REFERENCE: CGC2046
; CURRENT APPLICATION NUMBER: US/09/415.522A
; CURRENT FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2071
; TYPE: PRT
; ORGANISM: Ashbya gossypii
US-09-415-522-6

Query Match 2.5%; Score 7; DB 3; Length 2071;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 SSPNSKN 143
Db 48 SSPNSKN 54
|||||

RESULT 41
US-09-628-665-13
; Sequence 13, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628.665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-13

Query Match 2.1%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 SRSQHS 162
Db 1 SRSQHS 6
|||||

RESULT 42
US-09-628-665-31
; Sequence 31, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831

; CURRENT APPLICATION NUMBER: US/09/628.665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-31

Query Match 2.1%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 SRSQHS 162
Db 3 SRSQHS 8
|||||

RESULT 43
US-09-612-402B-26
; Sequence 26, Application US/09612402B
; Patent No. 6642023
; GENERAL INFORMATION:
; APPLICANT: Jackson, W. James
; APPLICANT: Pace, John
; TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
; FILE REFERENCE: 7969-086-999
; CURRENT APPLICATION NUMBER: US/09/612.402B
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/942,596
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Chlamydia sp.
US-09-612-402B-26

Query Match 2.1%; Score 6; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 LSNLHL 169
Db 8 LSNLHL 13
|||||

RESULT 44
US-09-030-619-50
; Sequence 50, Application US/09030619B
; Patent No. 6503881
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erffle, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 66081.406
; CURRENT APPLICATION NUMBER: US/09/030.619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0

```
; SEQ ID NO. 50
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indolicidin Analogue
US-09-030-619-50

Query Match          2.1%; Score 6; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      89 RKWILR 94
Db      11 RKWILR 16

RESULT 45
US-08-858-207A-268
; Sequence 268, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Stodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017670
; FILING DATE: 14-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50475
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 268:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6348328e
US-08-858-207A-268

Query Match          2.1%; Score 6; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38 FTNELK 43
Db      19 FTNELK 24

RESULT 46
US-09-328-352-6548
; Sequence 6548, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6548
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6548

Query Match          2.1%; Score 6; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      54 IACFLK 59
Db      1 IACFLK 6

RESULT 47
US-09-107-532A-5502
; Sequence 5502, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5502:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
```



```

;
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...78
; SEQUENCE DESCRIPTION: SEQ ID NO: 5502:
US-09-107-532A-5502

Query Match      2.1%; Score 6; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      68 NDEESM 73
Db      21 NDEESM 26

RESULT 48
US-09-543-681A-5440
; Sequence 5440, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5440
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5440

Query Match      2.1%; Score 6; DB 4; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      86 QLVKRM 91
Db      51 QLVKRM 56

RESULT 49
US-09-328-352-5745
; Sequence 5745, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5745
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5745

Query Match      2.1%; Score 6; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 IVIFTV 24
Db      16 IVIFTV 21

RESULT 50
US-08-946-329A-99
; Sequence 99, Application US/08946329A
; Patent No. 6057091
; GENERAL INFORMATION:
; APPLICANT: Beachy, Philip A.
; APPLICANT: Porter, Jeffrey A.
; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,329A
; FILING DATE: 07-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,323
; FILING DATE: 07-OCT-1996
; APPLICATION NUMBER: 08/729,743
; FILING DATE: 10-JUL-1996
; APPLICATION NUMBER: 08/567,357
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/349,498
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-946-329A-99

Query Match      2.1%; Score 6; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      170 RNGLV 175
Db      44 RNGLV 49

RESULT 51
US-09-543-681A-8267
; Sequence 8267, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAB
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8267
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Proteus mirabilis

```

US-09-543-681A-8267

Query Match 2.1%; Score 6; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 162 SFLSNL 167
Db 3 SFLSNL 8

RESULT 52

US-08-822-830B-4
; Sequence 4, Application US/08822830B
; Patent No. 5871734
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.; Burkly, Linda C.
; TITLE OF INVENTION: Treatment for Asthma with VLA-4 Blocking
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-MAR-1997
APPLICATION NUMBER: US/08/822,830B
PRIOR APPLICATION DATA:
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: US 08/456,193

PRIOR APPLICATION DATA:
FILING DATE: 12-FEB-1992
APPLICATION NUMBER: US 07/835,139

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (PLM)

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: BGP-021USCN

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 4:

LENGTH: 106 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-822-830B-4

Query Match 2.1%; Score 6; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 TISTVQ 104
Db 74 TISTVQ 79

RESULT 53

US-08-950-660-4
; Sequence 4, Application US/08950660
; Patent No. 5932214
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.; Burkly, Linda C.
; TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 08/08/950,660
APPLICATION NUMBER: US/08/950,660

PRIOR APPLICATION DATA:
FILING DATE: 08/456,124

APPLICATION NUMBER: 08/456,124

FILING DATE: 18-JAN-1995

APPLICATION NUMBER: US 08/373,857

PRIOR APPLICATION DATA:
FILING DATE: 11-AUG-1994

APPLICATION NUMBER: US 08/284,603

PRIOR APPLICATION DATA:
FILING DATE: 02-FEB-1993

APPLICATION NUMBER: PCT/US93/00924

PRIOR APPLICATION DATA:
FILING DATE: 07/835,139

APPLICATION NUMBER: US 07/835,139

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (PLM)

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: BGP-031USCP2

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 4:

LENGTH: 106 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-950-660-4

Query Match 2.1%; Score 6; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 TISTVQ 104
Db 74 TISTVQ 79

RESULT 54

US-09-157-452B-4
; Sequence 4, Application US/09157452B
; Patent No. 6482409
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; APPLICANT: Burkly, Linda C.
; TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
; FILE REFERENCE: 10274-004003
; CURRENT APPLICATION NUMBER: US/09/157,452B
; CURRENT FILING DATE: 1998-09-21

; PRIOR APPLICATION NUMBER: US 08/950,660
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 08/373,857
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/284,603
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: PCT/US93/00924
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: US 07/835,139
; PRIOR FILING DATE: 1992-02-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-157-452B-4

Query Match 2.1%; Score 6; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 T1STVQ 104
Db 74 T1STVQ 79

RESULT 55
US-08-454-899G-10
; Sequence 10, Application US/08454899G
; Patent No. 6602503
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; APPLICANT: Carr, Philip J.
; APPLICANT: Tempest, Philip R.
; TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
; FILE REFERENCE: 10274-007001
; CURRENT APPLICATION NUMBER: US/08/454,899G
; CURRENT FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/004,798
; PRIOR FILING DATE: 1993-01-12
; PRIOR APPLICATION NUMBER: PCT/US94/00266
; PRIOR FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region
US-08-454-899G-10

Query Match 2.1%; Score 6; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 T1STVQ 104
Db 74 T1STVQ 79

RESULT 56
PCT-US93-00030-4
; Sequence 4, Application PC/TUS9300030
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; TITLE OF INVENTION: Treatment for Asthma
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago

; STATE: IL
; COUNTRY: US
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00030
; FILING DATE: 19930112
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 92,307-A; D002 CIP PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-00030-4

Query Match 2.1%; Score 6; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 T1STVQ 104
Db 74 T1STVQ 79

RESULT 57
PCT-US93-00924-4
; Sequence 4, Application PC/TUS9300924
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; TITLE OF INVENTION: Treatment for Inflammatory Bowel Disease
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00924
; FILING DATE: 19930202
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 92,308-A; D003 CIP PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-00924-4

Query Match 2.1%; Score 6; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 T1STVQ 104
Db 74 T1STVQ 79

RESULT 58
US-09-621-976-5264
; Sequence 5264, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5264
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -14...-1
; NAME/KEY: UNSURE
; LOCATION: 47
; OTHER INFORMATION: Xaa = Ala,Ser,Thr
; NAME/KEY: UNSURE
; LOCATION: 2,40
; OTHER INFORMATION: Xaa = Ala,Thr
; NAME/KEY: UNSURE
; LOCATION: 71
; OTHER INFORMATION: Xaa = Arg,Ser
; NAME/KEY: UNSURE
; LOCATION: 3
; OTHER INFORMATION: Xaa = Asp,Gly
; NAME/KEY: UNSURE
; LOCATION: 80
; OTHER INFORMATION: Xaa = Cys,Tyr
; NAME/KEY: UNSURE
; LOCATION: 4
; OTHER INFORMATION: Xaa = Gly,Ser
; NAME/KEY: UNSURE
; LOCATION: 8
; OTHER INFORMATION: Xaa = His,Gln
; NAME/KEY: UNSURE
; LOCATION: 70
; OTHER INFORMATION: Xaa = His,Gln,Arg
; NAME/KEY: UNSURE
; LOCATION: 62
; OTHER INFORMATION: Xaa = Pro,Gln
; NAME/KEY: UNSURE
; LOCATION: 61
; OTHER INFORMATION: Xaa = Pro,Thr

US-09-621-976-5264

Query Match 2.1%; Score 6; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 QRVAH 125
Db 37 QRVAH 42

RESULT 59

US-09-134-001C-5132
; Sequence 5132, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5132
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5132

Query Match 2.1%; Score 6; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 IYQGGI 247
Db 83 IYQGGI 88

RESULT 60
US-09-489-039A-9835
; Sequence 9835, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9835
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9835

Query Match 2.1%; Score 6; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 NISPLV 114
Db 6 NISPLV 11

RESULT 61
US-08-635-886C-248
; Sequence 248, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555

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; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 119
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-248

Query Match          2.1%; Score 6; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 GAFLVG 281
Db      83 GAFLVG 88

RESULT 62
US-08-974-690C-248
; Sequence 248, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 119
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-248

Query Match          2.1%; Score 6; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 GAFLVG 281
Db      83 GAFLVG 88

RESULT 63
US-08-635-886C-240
; Sequence 240, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 240
; LENGTH: 128
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-240

Query Match          2.1%; Score 6; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 GAFLVG 281
Db      92 GAFLVG 97

RESULT 64
US-08-974-690C-240
; Sequence 240, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 128
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-240

Query Match          2.1%; Score 6; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 GAFLVG 281
Db      92 GAFLVG 97

RESULT 65
US-09-134-000C-3666
; Sequence 3666, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3666
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3666

Query Match          2.1%; Score 6; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 116 ERGPQR 121
 Db 59 ERGPQR 64

RESULT 66

US-09-252-991A-18565
 ; Sequence 18565, Application US/09252991A
 ; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 18565

; LENGTH: 134

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-18565

Query Match 2.1%; Score 6; DB 4; Length 134;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TGTGR 132
 Db 50 TGTGR 55

RESULT 67

US-09-252-991A-22722
 ; Sequence 22722, Application US/09252991A
 ; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 22722

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22722

Query Match 2.1%; Score 6; DB 4; Length 135;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 PNDEES 72
 Db 40 PNDEES 45

RESULT 68

US-09-252-991A-27904
 ; Sequence 27904, Application US/09252991A
 ; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 27904

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27904

Query Match

2.1%; Score 6; DB 4; Length 135;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 GTRGRS 133
 Db 69 GTRGRS 74

RESULT 69

US-09-328-352-4265

; Sequence 4265, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 4265

; LENGTH: 137

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-4265

Query Match

2.1%; Score 6; DB 4; Length 137;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 ERGPQR 121
 Db 101 ERGPQR 106

RESULT 70

US-09-134-001C-3776

; Sequence 3776, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3776

; LENGTH: 138

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3776

Query Match 2.1%; Score 6; DB 4; Length 138;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 KNEKAL 147
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 Db 15 KNEKAL 20

RESULT 71

US-09-134-000C-6375
 ; Sequence 6375, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6375
 ; LENGTH: 140
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis

US-09-134-000C-6375

Query Match 2.1%; Score 6; DB 4; Length 140;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 ETISTV 103
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 Db 34 ETISTV 39

RESULT 72

US-09-593-887-8
 ; Sequence 8, Application US/09593887
 ; Patent No. 6607914
 ; GENERAL INFORMATION:
 ; APPLICANT: Belyavsky, Alexander
 ; APPLICANT: Popsueva, Anna
 ; APPLICANT: Luchinskaya, Natalia
 ; TITLE OF INVENTION: CAMELLO GENE FAMILY AND USES THEREOF
 ; FILE REFERENCE: 63475/258
 ; CURRENT APPLICATION NUMBER: US/09/593,887
 ; CURRENT FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: US 09/333,229
 ; PRIOR FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-593-887-8

Query Match 2.1%; Score 6; DB 4; Length 144;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 KALGRK 150
 |||||
 Db 101 KALGRK 106

RESULT 73

US-09-134-001C-3901
 ; Sequence 3901, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 3901
 ; LENGTH: 145
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3901

Query Match 2.1%; Score 6; DB 4; Length 145;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 259 SVTNEH 264
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 Db 65 SVTNEH 70

RESULT 74

US-09-461-325-458
 ; Sequence 458, Application US/09461325A
 ; Patent No. 6475753
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 94 Human Secreted Proteins
 ; FILE REFERENCE: P2029P1
 ; CURRENT APPLICATION NUMBER: US/09/461,325A
 ; CURRENT FILING DATE: 1999-12-14
 ; EARLIER APPLICATION NUMBER: PCT/US99/13418
 ; EARLIER FILING DATE: 1999-06-15
 ; EARLIER APPLICATION NUMBER: 60/089,507
 ; EARLIER FILING DATE: 1998-06-16
 ; EARLIER APPLICATION NUMBER: 60/089,508
 ; EARLIER FILING DATE: 1998-06-16
 ; EARLIER APPLICATION NUMBER: 60/089,509
 ; EARLIER FILING DATE: 1998-06-16
 ; EARLIER APPLICATION NUMBER: 60/089,510
 ; EARLIER FILING DATE: 1998-06-16
 ; EARLIER APPLICATION NUMBER: 60/090,112
 ; EARLIER FILING DATE: 1998-06-22
 ; EARLIER APPLICATION NUMBER: 60/090,113
 ; NUMBER OF SEQ ID NOS: 532
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 458
 ; LENGTH: 147
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-461-325-458

Query Match 2.1%; Score 6; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 128 GTRGRS 133
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 Db 43 GTRGRS 48

RESULT 75

US-10-012-542-458

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; Sequence 458, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 458
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-542-458
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Query Match          2.1%; Score 6; DB 4; Length 147;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 128 GTRGRS 133
    |||||
Db 43 GTRGRS 48
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Job time : 25 secs
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:23:46 ; Search time 46 Seconds
(without alignments)

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Title: US-10-662-429-2

Perfect score: 281

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10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubaa/US09C_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	281	100.0	281	8	US-08-971-317A-8
3	281	100.0	281	9	US-08-813-329-17
4	281	100.0	281	9	US-08-133-663-8
5	281	100.0	281	9	US-09-934-465-1
6	281	100.0	281	10	US-09-919-039-118
7	281	100.0	281	12	US-10-202-062-20
8	281	100.0	281	12	US-10-662-429-2
9	281	100.0	281	12	US-10-662-430-2
10	281	100.0	281	12	US-10-862-431-2
11	281	100.0	281	13	US-10-039-785-66
12	281	100.0	281	13	US-10-011-125-4
13	281	100.0	281	13	US-10-001-054-54
14	281	100.0	281	14	US-10-093-766-54
15	281	100.0	281	14	US-10-174-654-11
					Sequence 6, Appli
					Sequence 8, Appli
					Sequence 17, Appli
					Sequence 18, Appli
					Sequence 1, Appli
					Sequence 118, Appli
					Sequence 20, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 66, Appli
					Sequence 4, Appli
					Sequence 54, Appli
					Sequence 54, Appli
					Sequence 11, Appli

16	281	100.0	281	14	US-10-151-882-41	Sequence 41, Appli
17	281	100.0	281	14	US-10-218-547-20	Sequence 20, Appli
18	281	100.0	281	14	US-10-322-673-72	Sequence 72, Appli
19	281	100.0	281	14	US-10-139-785-66	Sequence 66, Appli
20	281	100.0	281	14	US-10-310-793-26	Sequence 26, Appli
21	281	100.0	281	15	US-10-292-486-5	Sequence 5, Appli
22	281	100.0	281	15	US-10-333-712-1	Sequence 1, Appli
23	279	99.3	279	13	US-10-066-209-3	Sequence 3, Appli
24	193	68.7	208	9	US-09-855-544A-16	Sequence 16, Appli
25	187	66.5	461	12	US-10-389-223A-6	Sequence 6, Appli
26	187	66.5	480	12	US-10-389-223A-4	Sequence 4, Appli
27	187	66.5	614	12	US-10-389-223A-2	Sequence 2, Appli
28	168	59.8	168	9	US-09-900-530A-10	Sequence 10, Appli
29	166	59.1	166	9	US-09-779-050A-16	Sequence 16, Appli
30	161	57.3	161	14	US-10-216-074-7	Sequence 7, Appli
31	161	57.3	161	14	US-10-338-083-11	Sequence 11, Appli
32	156	55.5	236	14	US-10-185-425-5	Sequence 5, Appli
33	141	50.2	246	9	US-09-855-544A-13	Sequence 13, Appli
34	127	45.2	164	13	US-10-116-378-29	Sequence 29, Appli
35	107	38.1	113	9	US-09-855-544A-15	Sequence 15, Appli
36	105	37.4	188	9	US-09-855-544A-14	Sequence 14, Appli
37	90	32.0	98	9	US-09-855-544A-10	Sequence 10, Appli
38	87	31.0	88	9	US-09-855-544A-9	Sequence 9, Appli
39	85	30.2	83	14	US-10-286-696-12	Sequence 12, Appli
40	56	19.9	56	15	US-10-399-018-20	Sequence 20, Appli
41	44	15.7	50	9	US-09-864-761-33427	Sequence 33427, A
42	44	15.7	52	9	US-09-855-544A-11	Sequence 11, Appli
43	44	15.7	55	9	US-09-855-544A-12	Sequence 12, Appli
44	34	12.1	34	14	US-10-272-411-24	Sequence 24, Appli
45	34	12.1	34	14	US-10-272-328A-24	Sequence 24, Appli
46	14	5.0	172	9	US-09-779-050A-17	Sequence 17, Appli
47	14	5.0	291	10	US-09-873-829-6	Sequence 6, Appli
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49	12	4.3	87	14	US-10-286-696-13	Sequence 13, Appli
50	11	3.9	21	15	US-10-399-018-21	Sequence 21, Appli
51	10	3.6	10	14	US-10-272-411-25	Sequence 25, Appli
52	10	3.6	10	14	US-10-272-328A-25	Sequence 25, Appli
53	9	3.2	9	14	US-10-272-411-27	Sequence 27, Appli
54	9	3.2	9	14	US-10-272-328A-27	Sequence 27, Appli
55	7	2.5	10	14	US-10-360-836-71	Sequence 71, Appli
56	7	2.5	42	12	US-10-424-599-25595	Sequence 25595, A
57	7	2.5	42	12	US-10-424-599-253624	Sequence 253624, A
58	7	2.5	60	12	US-10-424-599-258329	Sequence 258329, A
59	7	2.5	112	12	US-10-424-599-143535	Sequence 143535, A
60	7	2.5	112	12	US-10-424-599-186624	Sequence 186624, A
61	7	2.5	125	14	US-10-103-313-421	Sequence 421, Appli
62	7	2.5	170	12	US-10-424-599-235009	Sequence 235009, A
63	7	2.5	184	12	US-10-424-599-164595	Sequence 164595, A
64	7	2.5	196	12	US-10-425-114-64832	Sequence 64832, A
65	7	2.5	200	14	US-10-178-055-4	Sequence 4, Appli
66	7	2.5	209	14	US-10-178-055-2	Sequence 2, Appli
67	7	2.5	240	9	US-09-997-165-2	Sequence 2, Appli
68	7	2.5	241	9	US-09-925-301-1105	Sequence 1105, Appli
69	7	2.5	247	14	US-10-145-602-4	Sequence 4, Appli
70	7	2.5	267	12	US-10-424-599-276617	Sequence 276617, A
71	7	2.5	418	9	US-09-808-483-18	Sequence 18, Appli
72	7	2.5	420	15	US-10-369-493-1984	Sequence 1984, Appli
73	7	2.5	429	15	US-10-282-132A-54850	Sequence 54850, A
74	7	2.5	429	15	US-10-312-273-227	Sequence 227, Appli
75	7	2.5	429	15	US-10-289-762-189	Sequence 189, Appli
76	7	2.5	474	14	US-10-156-761-11437	Sequence 11437, A
77	7	2.5	531	12	US-10-425-114-46560	Sequence 46560, A
78	7	2.5	552	14	US-10-236-433-16	Sequence 16, Appli
79	7	2.5	574	14	US-10-236-433-2	Sequence 2, Appli
80	7	2.5	758	15	US-10-108-260A-2713	Sequence 2713, Appli
81	7	2.5	942	12	US-10-425-114-68187	Sequence 68187, A
82	7	2.5	1009	14	US-10-156-761-13813	Sequence 13813, A
83	7	2.5	1084	13	US-10-024-623-23	Sequence 23, Appli
84	7	2.5	1084	14	US-10-154-419-73	Sequence 73, Appli
85	7	2.5	1084	14	US-10-146-733-68	Sequence 68, Appli
86	7	2.5	1095	13	US-10-024-623-26	Sequence 26, Appli
87	7	2.5	1095	13	US-10-024-623-36	Sequence 36, Appli
88	7	2.5	1095	14	US-10-154-419-76	Sequence 76, Appli

89 7 2.5 1095 14 US-10-154-419-86 Sequence 85, Appl
 90 7 2.5 1095 14 US-10-146-733-71 Sequence 71, Appl
 91 7 2.5 1095 14 US-10-146-733-81 Sequence 81, Appl
 92 7 2.5 1847 15 US-10-369-493-1075 Sequence 1075, Ap
 93 7 2.5 1981 9 US-09-928-457-38 Sequence 38, Appl
 94 7 2.5 2015 12 US-10-282-122A-65772 Sequence 65772, A
 95 7 2.5 2015 14 US-10-066-551-1 Sequence 1, Appl
 96 6 2.1 6 14 US-10-272-411-26 Sequence 26, Appl
 97 6 2.1 6 14 US-10-272-328A-26 Sequence 26, Appl
 98 6 2.1 14 9 US-09-900-530A-19 Sequence 19, Appl
 99 6 2.1 22 9 US-09-864-761-34476 Sequence 34476, A
 100 6 2.1 23 10 US-09-776-724A-187 Sequence 187, App

ALIGNMENTS

RESULT 1
 US-08-916-625B-6
 ; Sequence 6, Application US/08916G25B
 ; Publication No. US20010010924A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DEEN, KRITH C.
 ; APPLICANT: YOUNG, PETER R.
 ; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
 ; TITLE OF INVENTION: RECEPTOR, TR6
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RATNER & PRESTIA
 ; STREET: P.O. BOX 980
 ; CITY: VALLEY FORGE
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/916.625B
 ; FILING DATE: 22-AUG-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/853.684
 ; FILING DATE: 09-MAY-1997
 ; APPLICATION NUMBER: 60/041,230
 ; FILING DATE: 14-MARCH-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PRESTIA, PAUL F
 ; REGISTRATION NUMBER: 23,031
 ; REFERENCE/DOCKET NUMBER: GH-50008-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0701
 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-916-625B-6

Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDQKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDQKYSKSGIACFLKE 60

QY 61 DDSYWDNDDESMNSPCQVKWQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DDSYWDNDDESMNSPCQVKWQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 QY 181 FYIYSOTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSAENSCWSKDAEYGLY 240
 DB 181 FYIYSOTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSAENSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 2
 US-08-971-317A-8
 ; Sequence 8, Application US/08971317A
 ; Publication No. US20010010925A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wiley, Steven R.
 ; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
 ; TITLE OF INVENTION: THEREOF
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FASTSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/971,317A
 ; FILING DATE: 17-NOV-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Goller, Mimi C
 ; REGISTRATION NUMBER: 39,046
 ; REFERENCE/DOCKET NUMBER: 6255.US.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (847) 935-7550
 ; TELEFAX: (847) 938-2623
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. US20010010925A1e
 ; US-08-971-317A-8

Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDQKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDQKYSKSGIACFLKE 60
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 DB 61 DDSYWDNDDESMNSPCQVKWQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGPO 120

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QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
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QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
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Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 3

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US-09-813-329-17
; Sequence 17, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/130,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-17
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Query Match 100.0%; Score 281; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGKIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGKIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEQQNISPVLVRGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEQQNISPVLVRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 4

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US-09-193-663-8
; Sequence 8, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255 US 02
; CURRENT APPLICATION NUMBER: US/09/193,663
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-8
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Query Match 100.0%; Score 281; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGKIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGKIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEQQNISPVLVRGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEQQNISPVLVRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
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Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 5

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US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1
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Query Match 100.0%; Score 281; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGKIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGKIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEQQNISPVLVRGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEQQNISPVLVRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 6

US-09-919-039-118
; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR FILING DATE: 2002-07-25
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118

Query Match 100.0%; Score 281; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSETISTVQEKQNIPLVREGRGP 120
Db 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSETISTVQEKQNIPLVREGRGP 120
Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7

US-10-202-062-20
; Sequence 20, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR FILING DATE: 2002-07-25
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-202-062-20

Query Match 100.0%; Score 281; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSETISTVQEKQNIPLVREGRGP 120
Db 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSETISTVQEKQNIPLVREGRGP 120
Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8

US-10-662-429-2
; Sequence 2, Application US/10662429
; Publication No. US20040038347A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,429
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-429-2

Query Match 100.0%; Score 281; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
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Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
Db 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
Qy 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 9

US-10-662-430-2
; Sequence 2, Application US/10662430
; Publication No. US20040048340A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,430
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 100.0%; Score 281; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
Db 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120

Qy 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 10

US-10-662-431-2
; Sequence 2, Application US/10662431
; Publication No. US20040047864A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,431
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 100.0%; Score 281; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
Db 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
Qy 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 11

US-10-039-785-66
; Sequence 66, Application US/10039785
; Publication No. US2002067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-66

Query Match 100.0%; Score 281; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANMEVGGPSLGGTCTVLIVFTVLLQSLCVAVTYVFTNELKQMDQKYSKSGIACFLKE 60
Db 1 MANMEVGGPSLGGTCTVLIVFTVLLQSLCVAVTYVFTNELKQMDQKYSKSGIACFLKE 60
QY 61 DDSYDPNDEESMNSPCQVQWQVLRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYDPNDEESMNSPCQVQWQVLRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 12

US-10-011-125-4

; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: F1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4

Query Match 100.0%; Score 281; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANMEVGGPSLGGTCTVLIVFTVLLQSLCVAVTYVFTNELKQMDQKYSKSGIACFLKE 60
Db 1 MANMEVGGPSLGGTCTVLIVFTVLLQSLCVAVTYVFTNELKQMDQKYSKSGIACFLKE 60
QY 61 DDSYDPNDEESMNSPCQVQWQVLRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYDPNDEESMNSPCQVQWQVLRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 13

US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Shelton, David
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29

1 PRIOR APPLICATION NUMBER: 60/085149
2 PRIOR FILING DATE: 1998-05-12
3 PRIOR APPLICATION NUMBER: 60/087607
4 PRIOR FILING DATE: 1998-06-02
5 PRIOR APPLICATION NUMBER: 60/088858
6 PRIOR FILING DATE: 1998-06-11
7 PRIOR APPLICATION NUMBER: 60/090691
8 PRIOR FILING DATE: 1998-06-25
9 PRIOR APPLICATION NUMBER: 60/096891
10 PRIOR FILING DATE: 1998-08-17
11 PRIOR APPLICATION NUMBER: 60/096894
12 PRIOR FILING DATE: 1998-08-17
13 PRIOR APPLICATION NUMBER: 60/099803
14 PRIOR FILING DATE: 1998-09-10
15 PRIOR APPLICATION NUMBER: 60/100263
16 PRIOR FILING DATE: 1998-09-14
17 PRIOR APPLICATION NUMBER: 60/100390
18 PRIOR FILING DATE: 1998-09-15
19 PRIOR APPLICATION NUMBER: 60/101476
20 PRIOR FILING DATE: 1998-09-23
21 PRIOR APPLICATION NUMBER: 60/107783
22 PRIOR FILING DATE: 1998-11-10
23 PRIOR APPLICATION NUMBER: 60/108849
24 PRIOR FILING DATE: 1998-11-18
25 PRIOR APPLICATION NUMBER: 60/112420
26 PRIOR FILING DATE: 1998-12-15
27 PRIOR APPLICATION NUMBER: 60/113296
28 PRIOR FILING DATE: 1998-12-22
29 PRIOR APPLICATION NUMBER: 60/115554
30 PRIOR FILING DATE: 1999-01-12
31 PRIOR APPLICATION NUMBER: 60/115558
32 PRIOR FILING DATE: 1999-01-12
33 PRIOR APPLICATION NUMBER: 60/116533
34 PRIOR FILING DATE: 1999-01-20
35 PRIOR APPLICATION NUMBER: 60/123618
36 PRIOR FILING DATE: 1999-03-10
37 PRIOR APPLICATION NUMBER: 60/131294
38 PRIOR FILING DATE: 1999-04-07
39 PRIOR APPLICATION NUMBER: 60/140650
40 PRIOR FILING DATE: 1999-06-22
41 PRIOR APPLICATION NUMBER: 60/141037
42 PRIOR FILING DATE: 1999-06-23
43 PRIOR APPLICATION NUMBER: 60/144758
44 PRIOR FILING DATE: 1999-07-20
45 PRIOR APPLICATION NUMBER: 60/162506
46 PRIOR FILING DATE: 1999-10-29
47 PRIOR APPLICATION NUMBER: 60/170262
48 PRIOR FILING DATE: 1999-12-09
49 PRIOR APPLICATION NUMBER: 60/187202
50 PRIOR FILING DATE: 2000-03-03
51 PRIOR APPLICATION NUMBER: 60/209832
52 PRIOR FILING DATE: 2000-06-05
53 PRIOR APPLICATION NUMBER: 60/232887
54 PRIOR FILING DATE: 2000-09-15
55 PRIOR APPLICATION NUMBER: 09/180997
56 PRIOR FILING DATE: 1998-11-19
57 PRIOR APPLICATION NUMBER: 09/218517
58 PRIOR FILING DATE: 1998-12-22
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61 PRIOR APPLICATION NUMBER: 09/380137
62 PRIOR FILING DATE: 1999-08-25
63 PRIOR APPLICATION NUMBER: 09/380138
64 PRIOR FILING DATE: 1999-08-25
65 PRIOR APPLICATION NUMBER: 09/380913
66 PRIOR FILING DATE: 1999-09-09
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68 PRIOR FILING DATE: 1999-10-18
69 PRIOR APPLICATION NUMBER: 09/423741
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71 PRIOR APPLICATION NUMBER: 09/709238
72 PRIOR FILING DATE: 2000-11-08
73 PRIOR APPLICATION NUMBER: 09/802706
74 PRIOR FILING DATE: 2001-03-09
75 PRIOR APPLICATION NUMBER: 09/866034
76 PRIOR FILING DATE: 2001-05-25
77 PRIOR APPLICATION NUMBER: 09/872035
78 PRIOR FILING DATE: 2001-06-01
79 PRIOR APPLICATION NUMBER: 09/882636
80 PRIOR FILING DATE: 2001-06-14
81 PRIOR APPLICATION NUMBER: 09/918585
82 PRIOR FILING DATE: 2001-07-30
83 PRIOR APPLICATION NUMBER: 09/924419
84 PRIOR FILING DATE: 2001-08-06
85 PRIOR APPLICATION NUMBER: 09/927796
86 PRIOR FILING DATE: 2001-08-06
87 PRIOR APPLICATION NUMBER: 09/929404
88 PRIOR FILING DATE: 2001-08-13
89 PRIOR APPLICATION NUMBER: 09/941992
90 PRIOR FILING DATE: 2001-08-28
91 PRIOR APPLICATION NUMBER: 09/946374
92 PRIOR FILING DATE: 2001-09-04
93 PRIOR APPLICATION NUMBER: PCT/US98/18824
94 PRIOR FILING DATE: 1998-09-10
95 PRIOR APPLICATION NUMBER: PCT/US99/00106
96 PRIOR FILING DATE: 1999-01-05
97 PRIOR APPLICATION NUMBER: PCT/US99/05028
98 PRIOR FILING DATE: 1999-03-08
99 PRIOR APPLICATION NUMBER: PCT/US99/08615
100 PRIOR FILING DATE: 1999-04-20
101 PRIOR APPLICATION NUMBER: PCT/US99/12252
102 PRIOR FILING DATE: 1999-06-02
103 PRIOR APPLICATION NUMBER: PCT/US99/20111
104 PRIOR FILING DATE: 1999-09-01
105 PRIOR APPLICATION NUMBER: PCT/US99/20594
106 PRIOR FILING DATE: 1999-09-08
107 PRIOR APPLICATION NUMBER: PCT/US99/28313
108 PRIOR FILING DATE: 1999-11-30
109 PRIOR APPLICATION NUMBER: PCT/US99/28551
110 PRIOR FILING DATE: 1999-12-02
111 PRIOR APPLICATION NUMBER: PCT/US99/28634
112 PRIOR FILING DATE: 1999-12-01
113 PRIOR APPLICATION NUMBER: PCT/US99/30095
114 PRIOR FILING DATE: 1999-12-16
115 PRIOR APPLICATION NUMBER: PCT/US99/30999
116 PRIOR FILING DATE: 1999-12-20
117 PRIOR APPLICATION NUMBER: PCT/US00/00376
118 PRIOR FILING DATE: 2000-01-06
119 PRIOR APPLICATION NUMBER: PCT/US00/03565
120 PRIOR FILING DATE: 2000-02-11
121 PRIOR APPLICATION NUMBER: PCT/US00/04341
122 PRIOR FILING DATE: 2000-02-18
123 PRIOR APPLICATION NUMBER: PCT/US00/04342
124 PRIOR FILING DATE: 2000-02-18
125 PRIOR APPLICATION NUMBER: PCT/US00/05841
126 PRIOR FILING DATE: 2000-03-02
127 PRIOR APPLICATION NUMBER: PCT/US00/06884
128 PRIOR FILING DATE: 2000-03-15
129 PRIOR APPLICATION NUMBER: PCT/US00/08439
130 PRIOR FILING DATE: 2000-03-30
131 PRIOR APPLICATION NUMBER: PCT/US00/13705
132 PRIOR FILING DATE: 2000-05-17
133 PRIOR APPLICATION NUMBER: PCT/US00/14042
134 PRIOR FILING DATE: 2000-05-22
135 PRIOR APPLICATION NUMBER: PCT/US00/14941
136 PRIOR FILING DATE: 2000-05-30
137 PRIOR APPLICATION NUMBER: PCT/US00/15264
138 PRIOR FILING DATE: 2000-06-02
139 PRIOR APPLICATION NUMBER: PCT/US00/22031
140 PRIOR FILING DATE: 2000-08-11
141 PRIOR APPLICATION NUMBER: PCT/US00/23522
142 PRIOR FILING DATE: 2000-08-23
143 PRIOR APPLICATION NUMBER: PCT/US00/30873
144 PRIOR FILING DATE: 2000-11-10
145 PRIOR APPLICATION NUMBER: PCT/US00/32678
146 PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: 2001-02-28
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 ; PRIOR FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/17092
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 ; PRIOR APPLICATION NUMBER: PCT/US01/17800
 ; PRIOR FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/19692
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: PCT/US01/21066
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: PCT/US01/21735
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: PCT/US01/27099
 ; PRIOR FILING DATE: 2001-08-29
 ; NUMBER OF SEQ ID NOS: 91
 ; SEQ ID NO 54
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-001-054-54

Query Match 100.0%; Score 281; DB 13; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DSYWDPNDESMNSPCQVQWQVQLVIRKMKILRTSEETISTVQEKQONISPLVREGPQ 120
 DB 61 DSYWDPNDESMNSPCQVQWQVQLVIRKMKILRTSEETISTVQEKQONISPLVREGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYDPDILLMKSARNCSWCKDAEYGLY 240
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYDPDILLMKSARNCSWCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14
 US-10-093-766-54
 ; Sequence 54, Application US/10093766
 ; Publication No. US20030013099A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lasek, Amy W.
 ; APPLICANT: Jones, David A.
 ; APPLICANT: Karpf, Adam R.
 ; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
 ; FILE REFERENCE: PA-0047 US
 ; CURRENT APPLICATION NUMBER: US/10/093,766
 ; CURRENT FILING DATE: 2002-03-07
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 54
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
 US-10-093-766-54

Query Match 100.0%; Score 281; DB 14; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DSYWDPNDESMNSPCQVQWQVQLVIRKMKILRTSEETISTVQEKQONISPLVREGPQ 120
 DB 61 DSYWDPNDESMNSPCQVQWQVQLVIRKMKILRTSEETISTVQEKQONISPLVREGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYDPDILLMKSARNCSWCKDAEYGLY 240
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYDPDILLMKSARNCSWCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 15
 US-10-174-654-11
 ; Sequence 11, Application US/10174654
 ; Publication No. US20030044937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bienkowski, Michael J
 ; Mills, Cynthia J
 ; Jones, David A
 ; TITLE OF INVENTION: TNF-Related Death Ligand
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
 ; STREET: 301 Henrietta Street
 ; CITY: Kalamazoo
 ; STATE: MI
 ; COUNTRY: USA
 ; ZIP: 49001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 Diskette
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/174,654
 ; FILING DATE: 19-Jun-2002
 ; CLASSIFICATION: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kerber, Lori L.
 ; REGISTRATION NUMBER: 41,113
 ; REFERENCE/DOCKET NUMBER: 6111.N CN1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 616/833-0974
 ; TELEFAX: 616/833-8897
 ; TELEX: 224401
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-10-174-654-11

Query Match 100.0%; Score 281; DB 14; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Db 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
QY 181 FYIYISQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYISQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 16

US-10-151-882-41
; Sequence 41, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-41

Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Db 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
QY 181 FYIYISQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYISQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 17

US-10-218-547-20
; Sequence 20, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha

; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-218-547-20

Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Db 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
QY 181 FYIYISQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYISQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 18

US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-72

Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DSDYNDPDEESMNSPCQVKQLRQVVKMLRTSEETISTVQEKQNI SPLVRERGPQ 120
Db 61 DSDYNDPDEESMNSPCQVKQLRQVVKMLRTSEETISTVQEKQNI SPLVRERGPQ 120
QY 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYISQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281

RESULT 19

US-10-139-785-66
; Sequence 66, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.

; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to TRAIL

; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-66

Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DSDYNDPDEESMNSPCQVKQLRQVVKMLRTSEETISTVQEKQNI SPLVRERGPQ 120
Db 61 DSDYNDPDEESMNSPCQVKQLRQVVKMLRTSEETISTVQEKQNI SPLVRERGPQ 120
QY 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Db 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYISQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281

RESULT 20

US-10-310-793-26
; Sequence 26, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping

; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Disease:
; Relating To Human Tumor Necrosis Factor-Gamma Beta

; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-310-793-26

Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DSDYNDPDEESMNSPCQVKQLRQVVKMLRTSEETISTVQEKQNI SPLVRERGPQ 120
Db 61 DSDYNDPDEESMNSPCQVKQLRQVVKMLRTSEETISTVQEKQNI SPLVRERGPQ 120
QY 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240

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Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYGGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYGGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 21
US-10-292-486-5
; Sequence 5, Application US/10292486
; Publication No. US20030228309A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
; FILE REFERENCE: PF532P1
; CURRENT APPLICATION NUMBER: US/10/292,486
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/403,376
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/377,973
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/331,309
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/986,149
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,359
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/295,018
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/252,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/248,847
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/246,612
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-486-5

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Query Match 100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLQGTCLVIFVTLVQLSCLVAVTYVYFTNELKQMDQKYSKGIACFLKE 60
Db 1 MAMMEVQGGPSLQGTCLVIFVTLVQLSCLVAVTYVYFTNELKQMDQKYSKGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLILTSSETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLILTSSETISTVQEKQONISPLVRERGPO 120

Qy 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
Db 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180

Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYGGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYGGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281

```

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RESULT 22
US-10-333-712-1
; Sequence 1, Application US/10333712
; Publication No. US20040005314A1
; GENERAL INFORMATION:
; APPLICANT: Escandon, Enrique

```

```

; APPLICANT: Fox, Judith A.
; APPLICANT: Kelley, Sean K.
; APPLICANT: Xiang, Hong
; TITLE OF INVENTION: APO-2L RECEPTOR AGONIST AND CPT-11 SYNERGISM
; FILE REFERENCE: P1838R1
; CURRENT APPLICATION NUMBER: US/10/333,712
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: PCT/US01/23691
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,256
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-333-712-1

Query Match 100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLQGTCLVIFVTLVQLSCLVAVTYVYFTNELKQMDQKYSKGIACFLKE 60
Db 1 MAMMEVQGGPSLQGTCLVIFVTLVQLSCLVAVTYVYFTNELKQMDQKYSKGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLILTSSETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLILTSSETISTVQEKQONISPLVRERGPO 120

Qy 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
Db 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180

Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYGGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYGGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281

```

```

RESULT 23
US-10-066-209-3
; Sequence 3, Application US/10066209
; Publication No. US20020115110A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030-D1
; CURRENT APPLICATION NUMBER: US/10/066,209
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/072,993
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-066-209-3

Query Match 99.3%; Score 279; DB 13; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.2e-271;

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Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVQGSLSGTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKGIACFLKEDD 62
DB 1 MMEVQGSLSGTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKGIACFLKEDD 60

QY 63 SYWDPNDESMNSPCQVQKWLRLVVRKMLRTSEETISTVQEKQONISPLVRERGPQRV 122
DB 61 SYWDPNDESMNSPCQVQKWLRLVVRKMLRTSEETISTVQEKQONISPLVRERGPQRV 120

QY 123 AAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKGFY 182
DB 121 AAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKGFY 180

QY 183 YIYSQTYFRFQBEIEKNTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEGLYSI 242
DB 181 YIYSQTYFRFQBEIEKNTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEGLYSI 240

QY 243 YGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 YGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFLVG 279

RESULT 24
US-09-855-544A-16
; Sequence 16, Application US/09855544A
; Patent No. US2002006125A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-16

Query Match 68.7%; Score 193; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.4e-185;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGSLSGTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKGIACFLKE 60
DB 1 MAMMEVQGSLSGTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKGIACFLKE 60

QY 61 DSYWDPNDESMNSPCQVQKWLRLVVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DSYWDPNDESMNSPCQVQKWLRLVVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180

QY 181 FYIYSQTYFRFQ 193
DB 181 FYIYSQTYFRFQ 193

RESULT 25
US-10-389-223A-6
; Sequence 6, Application US/10389223A
; Publication No. US20040033511A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wuest, Harald
; APPLICANT: Moosmayer, Dieter
; TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytokines
; TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)

FILE REFERENCE: 1708.002US1
CURRENT APPLICATION NUMBER: US/10/389,223A
CURRENT FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 461
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of sequence 6: synthetic amino acid sequence of an anti-body-cytokine AMAIZE fusion protein of the invention exempl
OTHER INFORMATION: TRAIL-AMAIZE (40)
FEATURE:
OTHER INFORMATION: Stop codon: NT 1384-1386
US-10-389-223A-6

Query Match 66.5%; Score 187; DB 12; Length 461;
Best Local Similarity 100.0%; Pred. No. 7.1e-179;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 154
DB 275 TSEETISTVQEKQONISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 334

QY 155 ESSRSGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFQBEIEKNTKNDKQVQYIYKYT 214
DB 335 ESSRSGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFQBEIEKNTKNDKQVQYIYKYT 394

QY 215 SYDPILLMKSARNSCWSDAEGLYSIYGGIFELKENDRIFFSVTNEHLIDMDHEASF 274
DB 395 SYDPILLMKSARNSCWSDAEGLYSIYGGIFELKENDRIFFSVTNEHLIDMDHEASF 454

QY 275 FGAEFLVG 281
DB 455 FGAEFLVG 461

RESULT 26
US-10-389-223A-4
; Sequence 4, Application US/10389223A
; Publication No. US20040033511A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wajant, Harald
; APPLICANT: Moosmayer, Dieter
; TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytokines
; TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
; FILE REFERENCE: 1708.002US1
; CURRENT APPLICATION NUMBER: US/10/389,223A
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of sequence 4: synthetic amino acid sequence of an anti-body-cytokine AMAIZE fusion protein of the invention exempl
OTHER INFORMATION: TRAIL-AMAIZE (OS4)
FEATURE:
OTHER INFORMATION: Stop codon: NT 1441-1443
US-10-389-223A-4

Query Match 66.5%; Score 187; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 7.3e-179;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 154
DB 294 TSEETISTVQEKQONISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 353

155 ESSRSGHSFLNLHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYT 214
156 |
354 ESSRSGHSFLNLHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYT 413
355 |
215 SYDPDILLMKSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
216 |
414 SYDPDILLMKSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 473
415 |
275 FGAFVLG 281
276 |
474 FGAFVLG 480
475 |
RESULT 27
US-10-389-223A-2
; Sequence 2, Application US/10389223A
; Publication No. US20040033511A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wajant, Harald
; APPLICANT: Wuest, Thomas
; APPLICANT: Moosmayer, Dieter
; TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytokines
; TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
; FILE REFERENCE: 1708.002US1
; CURRENT APPLICATION NUMBER: US/10/389,223A
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 2
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of sequence 2: synthetic amino acid sequence of an
; OTHER INFORMATION: anti-body-cytokine AMAIZE fusion protein of the invention exempl
; OTHER INFORMATION: TRAIL-AMAIZE (MBOS4)
; FEATURE:
; OTHER INFORMATION: Stop codon: NT 1843-1845
US-10-389-223A-2
Query Match 66.5%; Score 187; DB 12; Length 614;
Best Local Similarity 100.0%; Pred. No. 9.1e-179;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 95 TSEETISVQEQKQNISPLVREGRGQVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 154
Qy 428 TSEETISVQEQKQNISPLVREGRGQVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 487
Qy 155 ESSRSGHSFLNLHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYT 214
Qy 488 ESSRSGHSFLNLHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYT 547
Qy 215 SYDPDILLMKSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Qy 548 SYDPDILLMKSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 607
Qy 275 FGAFVLG 281
Qy 608 FGAFVLG 614
RESULT 28
US-09-900-530A-10
; Sequence 10, Application US/09900530A
; Patent No. US20020128438A1
; GENERAL INFORMATION:
; APPLICANT: Seol, Dae-Wu
; APPLICANT: Billiar, Timothy R.
; TITLE OF INVENTION: DNA Cassette for the Production of
; TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline
; TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated Virus Vector, Their

; TITLE OF INVENTION: Combination and Use in Gene Therapy
; FILE REFERENCE: 5006-1-002
; CURRENT APPLICATION NUMBER: US/09/900,530A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: KR 2000-38441
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-900-530A-10
Query Match 59.8%; Score 168; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.4e-160;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 114 VREGRQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESRSGHSFLNLHLRNGE 173
Qy 174 LVTHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSDPILLMKSARNSCWSK 233
Qy 61 LVTHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSDPILLMKSARNSCWSK 120
Qy 234 DAEGYLSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Qy 121 DAEGYLSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 168
RESULT 29
US-09-779-050A-16
; Sequence 16, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 16
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-16
Query Match 59.1%; Score 166; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.4e-158;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 116 ERGQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESRSGHSFLNLHLRNGELV 175
Qy 176 IHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSDPILLMKSARNSCWSKDA 235
Qy 61 IHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSDPILLMKSARNSCWSKDA 120
Qy 236 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Qy 121 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 166
RESULT 30
US-10-216-074-7
; Sequence 7, Application US/10216074
; Publication No. US2003014845A1

```
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-7

Query Match      57.3%; Score 161; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 3.5e-153;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 1 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 60

Qy 181 FYYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKSRNSCWDKAEYGLY 240
Db 61 FYYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKSRNSCWDKAEYGLY 120

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 161

RESULT 31
US-10-338-083-11
; Sequence 11, Application US/10338083
; Publication No. US20030166559A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-11

Query Match      57.3%; Score 161; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 3.5e-153;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 QRVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEK 179
Db 1 QRVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEK 60

Qy 180 GFYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKSRNSCWDKAEYGL 239
Db 61 GFYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKSRNSCWDKAEYGL 120
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Qy 240 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 280
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 161

RESULT 32
US-10-185-425-5
; Sequence 5, Application US/10185425
; Publication No. US20030053984A1
; GENERAL INFORMATION:
; APPLICANT: Apotech Research and Development Ltd.
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Holler, Nils
; TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
; TITLE OF INVENTION: Recombinant Fusion Proteins
; FILE REFERENCE: 1708.001US1
; CURRENT APPLICATION NUMBER: US/10/185,425
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: PCT/EP00/13032
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: DE 199 63 859.4
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TRAIL-ACRP30
; NAME/KEY: DOMAIN
; LOCATION: (1)...(8)
; OTHER INFORMATION: Flag
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (9)...(16)
; OTHER INFORMATION: Linker
; NAME/KEY: DOMAIN
; LOCATION: (17)...(108)
; OTHER INFORMATION: mouseACRP30 aa 18-111
; NAME/KEY: DOMAIN
; LOCATION: (109)...(110)
; OTHER INFORMATION: Linker
; NAME/KEY: DOMAIN
; LOCATION: (111)...(296)
; OTHER INFORMATION: humanTRAIL aa 95-281
US-10-185-425-5

Query Match      55.5%; Score 156; DB 14; Length 296;
Best Local Similarity 100.0%; Pred. No. 6.2e-148;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 ITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKGFYIY 185
Db 141 ITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKGFYIY 200

Qy 186 SOTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKSRNSCWDKAEYGLYSIYQG 245
Db 201 SOTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKSRNSCWDKAEYGLYSIYQG 260

Qy 246 GIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 261 GIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 296

RESULT 33
US-09-855-544A-13
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; Sequence 13, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-13

Query Match      50.2%; Score 141; DB 9; Length 246;
Best Local Similarity 100.0%; Pred. No. 5.9e-133;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      141 SKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVVIHEKGFYIYSOTYFRFOBEIKENT 200
Db      141 SKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVVIHEKGFYIYSOTYFRFOBEIKENT 165

Qy      201 KNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEYGLYSIYGGIFELKENDRIFSV 260
Db      201 KNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEYGLYSIYGGIFELKENDRIFSV 225

Qy      261 TNEHLIDMDHEASFFGAFVNG 281
Db      261 TNEHLIDMDHEASFFGAFVNG 246

RESULT 34
US-10-116-378-29
; Sequence 29, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206K1
; CURRENT APPLICATION NUMBER: US/10/116,378
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 29
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-29

Query Match      45.2%; Score 127; DB 13; Length 164;
Best Local Similarity 100.0%; Pred. No. 4.6e-119;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      118 GPQVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVVIH 177
Db      118 GPQVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVVIH 60

Qy      178 EKGFYIYSOTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEY 237
Db      61 EKGFYIYSOTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEY 120
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Qy      238 GLYSIQ 244
Db      121 GLYSIQ 127

RESULT 35
US-09-855-544A-15
; Sequence 15, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-15

Query Match      38.1%; Score 107; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9e-99;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MANMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
Db      1 MANMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Qy      61 DDSYDNDDEESMNSPCWQVKWLRLVVRKMLRTSEETISTVQEQ 107
Db      61 DDSYDNDDEESMNSPCWQVKWLRLVVRKMLRTSEETISTVQEQ 107

RESULT 36
US-09-855-544A-14
; Sequence 14, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-14

Query Match      37.4%; Score 105; DB 9; Length 188;
Best Local Similarity 100.0%; Pred. No. 6.2e-97;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MANMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
Db      1 MANMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Qy      61 DDSYDNDDEESMNSPCWQVKWLRLVVRKMLRTSEETISTVQEQ 105
Db      61 DDSYDNDDEESMNSPCWQVKWLRLVVRKMLRTSEETISTVQEQ 105

RESULT 37
US-09-855-544A-10
; Sequence 10, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
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; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-10

Query Match      32.0%; Score 90; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 4e-82;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCQWKQRLQRLVK 90
DB 61 DDSYWDNDDESMNSPCQWKQRLQRLVK 90

RESULT 38
US-09-855-544A-9
; Sequence 9, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-9

Query Match      31.0%; Score 87; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.7e-79;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCQWKQRLQRLVK 87
DB 61 DDSYWDNDDESMNSPCQWKQRLQRLVK 87

RESULT 39
US-10-286-696-12
; Sequence 12, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Heu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm. A No. US20030129706A1el Member of the TNF Ligand Super-gene
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
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; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-696-12

Query Match      30.2%; Score 85; DB 14; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.6e-77;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 ERGPQVAAHITGTCRSNTLSSPNSKNEKALCRKINSWESSRSGHSFSLNHLRNGELV 175
DB 1 ERGPQVAAHITGTCRSNTLSSPNSKNEKALCRKINSWESSRSGHSFSLNHLRNGELV 60
QY 176 IHEKGFYIYSQTYFRFOEIKENT 200
DB 61 IHEKGFYIYSQTYFRFOEIKENT 85

RESULT 40
US-10-399-018-20
; Sequence 20, Application US/10399018
; Publication No. US20040002118A1
; GENERAL INFORMATION:
; APPLICANT: Smilansky, Zeev
; TITLE OF INVENTION: METHOD FOR DETERMINING MASS ALTERING MOIETY IN PEPTIDES
; FILE REFERENCE: 9124.137USWO
; CURRENT APPLICATION NUMBER: US/10/399,018
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/IL01/00944
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: IL138946
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-018-20

Query Match      19.9%; Score 56; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.2e-48;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 RTSETISTVQEKQONISPLVRERGPQVAAHITGTCRSNTLSSPNSKNEKALGR 149
DB 1 RTSETISTVQEKQONISPLVRERGPQVAAHITGTCRSNTLSSPNSKNEKALGR 56

RESULT 41
US-09-864-761-33427
; Sequence 33427, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
```


PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33427
LENGTH: 50
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007051.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.97
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: P50591, EVALUE 3.00e-19
OTHER INFORMATION: EST HUMAN HIT: AUI34224.1, EVALUE 1.00e-18
OTHER INFORMATION: EST_HUMAN HIT: H54628.1, EVALUE 3.00e-18
US-09-864-761-33427

Query Match 15.7%; Score 44; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.2e-36;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQ 44
DB 2 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQ 45

RESULT 42
US-09-855-544A-11
Sequence 11, Application US/09855544A
Patent No. US20020061525A1
GENERAL INFORMATION:
APPLICANT: Rodrigo YELIN et al.
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REFERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
US-09-855-544A-11

Query Match 15.7%; Score 44; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.3e-36;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQ 44
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQ 44

RESULT 43
US-09-855-544A-12
Sequence 12, Application US/09855544A
Patent No. US20020061525A1
GENERAL INFORMATION:
APPLICANT: Rodrigo YELIN et al.
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REFERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 55
TYPE: PRT
ORGANISM: Homo sapiens
US-09-855-544A-12

Query Match 15.7%; Score 44; DB 9; Length 55;
Best Local Similarity 100.0%; Pred. No. 3.4e-36;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQ 44
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQ 44

RESULT 44
US-10-272-411-24
Sequence 24, Application US/10272411
Publication No. US20030100068A1
GENERAL INFORMATION:
APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFERENCE: 60019620-0202
CURRENT APPLICATION NUMBER: US/10/272,411
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-10-272-411-24

Query Match 12.1%; Score 34; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.4e-26;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TRGRSNTLSSPNSKNEKALGRKINSWESSRSGHS 162
DB 1 TRGRSNTLSSPNSKNEKALGRKINSWESSRSGHS 34

RESULT 45
US-10-272-328A-24
Sequence 24, Application US/10272328A
Publication No. US20030109444A1

```
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 24
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-328A-24

Query Match      12.1%; Score 34; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.4e-26;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      129 TGRSNTLSSNSKNEKALGRKINSWESSRSQHS 162
Db      1 TGRSNTLSSNSKNEKALGRKINSWESSRSQHS 34

RESULT 46
US-09-779-050A-17
; Sequence 17, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 17
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-17

Query Match      5.0%; Score 14; DB 9; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      207 VQIYKYTSYPDPI 220
Db      98 VQIYKYTSYPDPI 111

RESULT 47
US-09-829-6
; Sequence 6, Application US/09873829
; Publication No. US20030185820A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Yongwon
; APPLICANT: Wong, Brian
; APPLICANT: Josien, Regis
; APPLICANT: Steinman, Ralph
; TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
; INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAM
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
```

```
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/873,829
; FILING DATE: 04-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,115
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-200 CIP N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-873-829-6

Query Match      5.0%; Score 14; DB 10; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      207 VQIYKYTSYPDPI 220
Db      217 VQIYKYTSYPDPI 230

RESULT 48
US-10-017-910-6
; Sequence 6, Application US/10017910
; Publication No. US20020159970A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Yongwon
; APPLICANT: Wong, Brian
; APPLICANT: Josien, Regis
; APPLICANT: Steinman, Ralph
; TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
; INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAM
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/10/017,910
; FILING DATE: 14-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/447,035
; FILING DATE: 1999-11-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-017-910-6

Query Match 5.0%; Score 14; DB 13; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKYSYPDI 220
Db 217 VQYIYKYSYPDI 230

RESULT 49
US-10-286-696-13
; Sequence 13, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Hau, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. US20030129706A1 Member of the TNF Ligand Supergene
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mouse
US-10-286-696-13

Query Match 4.3%; Score 12; DB 14; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 YIYQTYFRFQE 194
Db 65 YIYQTYFRFQE 76

RESULT 50
US-10-399-018-21
; Sequence 21, Application US/10399018
; Publication No. US20040002118A1
; GENERAL INFORMATION:
; APPLICANT: Smilansky, Zeev
```

```
; TITLE OF INVENTION: METHOD FOR DETERMINING MASS ALTERING MOIETY IN PEPTIDES
; FILE REFERENCE: 9124.137USWO
; CURRENT APPLICATION NUMBER: US/10/399,018
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/IL01/00944
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: IL18946
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-018-21

Query Match 3.9%; Score 11; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 RTSETISTVQ 104
Db 1 RTSETISTVQ 11

RESULT 51
US-10-272-411-25
; Sequence 25, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-411-25

Query Match 3.6%; Score 10; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKENTKN 202
Db 1 QEEIKENTKN 10

RESULT 52
US-10-272-328A-25
; Sequence 25, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-328A-25

Query Match 3.6%; Score 10; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0;
Matches 10; Conservative 0; Mismatches 0; Gaps 0;

QY 193 QBEIKENTKN 202
Db 1 QBEIKENTKN 10
|||||

RESULT 53
US-10-272-411-27
; Sequence 27, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-411-27

Query Match 3.2%; Score 9; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 229 SCWSKDAEY 237
Db 1 SCWSKDAEY 9
|||||

RESULT 54
US-10-272-328A-27
; Sequence 27, Application US/10272328A
; Publication No. US2003010944A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-328A-27

Query Match 3.2%; Score 9; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 229 SCWSKDAEY 237
Db 1 SCWSKDAEY 9
|||||

RESULT 55
US-10-360-836-71
; Sequence 71, Application US/10360836
; Publication No. US20030185854A1
; GENERAL INFORMATION:
; APPLICANT: Zavala, Fidel
; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; TITLE OF INVENTION: AND MALIGNANCIES
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Plasmodium
US-10-360-836-71

Query Match 2.5%; Score 7; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 141 SKNEKAL 147
Db 2 SKNEKAL 8
|||||

RESULT 56
US-10-424-599-255595
; Sequence 255595, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 255595
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72823C.1.pep
US-10-424-599-255595

Query Match 2.5%; Score 7; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 194 EEIKENT 200
Db 12 EEIKENT 18
|||||

RESULT 57
US-10-424-599-263624

; Sequence 263624, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 263624
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80072C.1.pep
US-10-424-599-263624

Query Match 2.5%; Score 7; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 KRMILRT 95
Db 32 KRMILRT 38

RESULT 58
US-10-424-599-258329
; Sequence 258329, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 258329
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(60)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_75296C.1.pep
US-10-424-599-258329

Query Match 2.5%; Score 7; DB 12; Length 60;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 KALGRKI 151
Db 37 KALGRKI 43

RESULT 59
US-10-424-599-143535
; Sequence 143535, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143535
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100626C.1.pep
US-10-424-599-143535

Query Match 2.5%; Score 7; DB 12; Length 112;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 KNEKALG 148
Db 97 KNEKALG 103

RESULT 60
US-10-424-599-186624
; Sequence 186624, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 186624
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139534C.1.pep
US-10-424-599-186624

Query Match 2.5%; Score 7; DB 12; Length 117;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLRQLVR 89
Db 69 QLRQLVR 75

RESULT 61
US-10-103-313-421
; Sequence 421, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ07C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 421
; LENGTH: 125
; TYPE: PRT

ORGANISM: Homo sapiens
US-10-103-313-421

Query Match 2.5%; Score 7; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 HSFLSNL 167
Db 32 HSFLSNL 38

RESULT 62

US-10-424-599-235009
; Sequence 235009, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 235009
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_54241C.1.pep
US-10-424-599-235009

Query Match 2.5%; Score 7; DB 12; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 HSFLSNL 167
Db 127 HSFLSNL 133

RESULT 63

US-10-424-599-164595
; Sequence 164595, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 164595
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_119647C.1.pep
US-10-424-599-164595

Query Match 2.5%; Score 7; DB 12; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 PNSKNEK 145
Db 145 PNSKNEK 145

Db 118 PNSKNEK 124

RESULT 64

US-10-425-114-64832
; Sequence 64832, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64832
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4720-003-G12_FLI.pep
US-10-425-114-64832

Query Match 2.5%; Score 7; DB 12; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 SIYQGGI 247
Db 55 SIYQGGI 61

RESULT 65

US-10-178-055-4
; Sequence 4, Application US/10178055
; Publication No. US20030105008A1
; GENERAL INFORMATION:
; APPLICANT: Dutta, Anindya
; APPLICANT: Dhar, Suman
; TITLE OF INVENTION: GEMININ AND ORC3N INHIBIT REPLICATION OF HERPESVIRUSES, PAPILLOM
; TITLE OF INVENTION: AND POLYOMAVIRUSES
; FILE REFERENCE: B00801/70253(JRV/MXA)
; CURRENT APPLICATION NUMBER: US/10/178,055
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,963
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-178-055-4

Query Match 2.5%; Score 7; DB 14; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QBEIKEN 199
Db 9 QBEIKEN 15

RESULT 66

US-10-178-055-2
; Sequence 2, Application US/10178055
; Publication No. US20030105008A1
; GENERAL INFORMATION:

```
; APPLICANT: Dutta, Anindya
; APPLICANT: Dhar, Suman
; TITLE OF INVENTION: GEMININ AND ORC3N INHIBIT REPLICATION OF HERPESVIRUSES, PAPILLOMA
; TITLE OF INVENTION: AND POLYOMAVIRUSES
; FILE REFERENCE: B00801/70253(JRV/MXA)
; CURRENT APPLICATION NUMBER: US/16/178,055
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,963
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-178-055-2

Query Match      2.5%; Score 7; DB 14; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      193 QEEIKEN 199
      |||||
Db      9 QEEIKEN 15

RESULT 67
US-09-997-165-2
; Sequence 2, Application US/09997165
; Patent No. US2002014199A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Fanslow, William C.
; TITLE OF INVENTION: LIGAND FOR CD7 AND METHODS OF USE THEREOF
; FILE REFERENCE: 2913-US
; CURRENT APPLICATION NUMBER: US/09/997,165
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: PCT/US00/14612
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,450
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-997-165-2

Query Match      2.5%; Score 7; DB 9; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      134 NTLSSPN 140
      |||||
Db      231 NTLSSPN 237

RESULT 68
US-09-925-301-1105
; Sequence 1105, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1105
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1105

Query Match      2.5%; Score 7; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      193 QEEIKEN 199
      |||||
Db      41 QEEIKEN 47

RESULT 69
US-10-145-602-4
; Sequence 4, Application US/10145602
; Publication No. US20030171563A1
; GENERAL INFORMATION:
; APPLICANT: McNamara, Peter
; TITLE OF INVENTION: REGULATORS OF BACTERIAL VIRULENCE FACTOR EXPRESSION
; FILE REFERENCE: KCC 4766
; CURRENT APPLICATION NUMBER: US/10/145,602
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/291,917
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-145-602-4

Query Match      2.5%; Score 7; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      255 RIFVSVT 261
      |||||
Db      91 RIFVSVT 97

RESULT 70
US-10-424-599-276617
; Sequence 276617, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 276617
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91804C.1.pep
US-10-424-599-276617

Query Match      2.5%; Score 7; DB 12; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      161 HSFLSNL 167
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Db 146 HGFLSNL 152
|||||

RESULT 71

US-09-808-483-18
; Sequence 18, Application US/09808483
; Patent No. US20020001824A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Ligand-gated anion channels of insects
; FILE REFERENCE: Le A 34 397
; CURRENT APPLICATION NUMBER: US/09/808,483
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: DE 100 136 19.2
; PRIOR FILING DATE: 2000-03-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-808-483-18

Query Match 2.5%; Score 7; DB 9; Length 418;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 PILLMK 225
|||||
Db 411 PILLMK 417

RESULT 72

US-10-369-493-1984
; Sequence 1984, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1984
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1984

Query Match 2.5%; Score 7; DB 15; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 VAVTVY 37
|||||
Db 47 VAVTVY 53

RESULT 73

US-10-282-122A-54850
; Sequence 54850, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 54850
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54850

Query Match 2.5%; Score 7; DB 12; Length 429;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSQH 161
|||||
Db 248 ESSRSQH 254

RESULT 74

US-10-312-273-227
; Sequence 227, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9

; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 227
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-227

Query Match 2.5%; Score 7; DB 15; Length 429;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 155 ESSRSRGH 161
Db 248 ESSRSRGH 254
|||||

RESULT 75
US-10-289-762-189
; Sequence 189, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 189
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-189

Query Match 2.5%; Score 7; DB 15; Length 429;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 155 ESSRSRGH 161
Db 248 ESSRSRGH 254
|||||

Search completed: March 23, 2004, 09:23:27
Job time : 47 secs

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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:15:55 ; Search time 60 Seconds
(without alignments)
1323.264 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281
Sequence: 1 MAMMEVQGPSLGTCTVLV.....NEHLIDMDHRSFGAFLVG 281

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

A.Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	281	100.0	281	2	Aaw19777 Novel cyt
2	281	100.0	281	2	Aaw27134 Human Apo
3	281	100.0	281	2	Aaw19787 Human Apo
4	281	100.0	281	2	Aaw76829 Human TL2
5	281	100.0	281	2	Aaw56760 Human TRA
6	281	100.0	281	2	Aaw44354 Human AGP
7	281	100.0	281	2	Aay01517 Protein a
8	281	100.0	281	2	Aay27012 Human Apo
9	281	100.0	281	3	Aay81956 Human Apo
10	281	100.0	281	3	Aab24038 Human PRO
11	281	100.0	281	3	Aab08545 Amino aci
12	281	100.0	281	3	Aab28691 Human AGP
13	281	100.0	281	4	Aab50977 Human PRO
14	281	100.0	281	4	Aab67243 Human Apo
15	281	100.0	281	4	Aae11031 Human TNF
16	281	100.0	281	4	Aab48350 Human TL2
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18	281	100.0	281	5	ABG31630 Human TRA
19	281	100.0	281	5	Aau75062 Human TNF
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21	281	100.0	281	5	ABP51954 Human Apo
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23	281	100.0	281	5	Aau79593 Human TNF
24	281	100.0	281	6	Abg73861 Human Apo
25	281	100.0	281	6	Abu10205 Human Apo

26	281	100.0	281	6	ABU71443 Human neo
27	281	100.0	281	6	ABG72738 Human TNF
28	281	100.0	281	6	AAO29543 Human TRA
29	281	100.0	281	6	ABU08558 Human TNF
30	281	100.0	281	6	ABR42313 Human TRA
31	281	100.0	281	6	ABG71905 Human TRA
32	281	100.0	281	6	ABP60546 Human tum
33	281	100.0	281	6	AAE36258 Human TRA
34	281	100.0	281	6	AAO31151 Human TNF
35	281	100.0	281	6	ABO25125 Human TNF
36	281	100.0	281	7	ADB61471 Native hu
37	281	100.0	281	7	ADC35202 Human TNF
38	281	100.0	281	7	ADD14080 Human src
39	281	100.0	281	7	ADD19010 Human dis
40	281	100.0	281	8	ADE76953 Human pro
41	279	99.3	279	8	AAW76332 Human TL2
42	279	99.3	279	2	AAW95032 Tumour ne
43	268	95.4	281	2	AAW27018 Human Apo
44	263	93.6	281	7	ADB61495 Human Apo
45	262	93.2	281	7	ADB61494 Human Apo
46	254	90.4	281	7	ADB61493 Human Apo
47	248	88.3	281	7	ADB61492 Human Apo
48	244	86.8	281	2	AAO15116 Protein a
49	242	86.1	266	4	AAW72935 OmpA sign
50	233	82.9	281	7	ADB61491 Human Apo
51	217	77.2	281	2	AAW27017 Human Apo
52	202	71.9	281	2	AAW27019 Human Apo
53	202	71.9	281	2	AAW27016 Human Apo
54	199	70.8	281	5	ABG72257 Human tra
55	193	68.7	212	5	AAU99301 Human TRA
56	187	66.5	253	4	AAE11037 GH-deriv
57	187	66.5	253	6	ABU08564 Human Gro
58	187	66.5	256	4	AAE11038 CMV-deriv
59	187	66.5	256	6	ABU08565 CMV sig.
60	187	66.5	461	5	AAO17496 Antibody-
61	187	66.5	480	5	AAO17495 Antibody-
62	187	66.5	614	3	AAO17494 Antibody-
63	186	66.2	441	3	AB28692 FC-huAGP-
64	185	65.8	281	7	ADB61476 Human Apo
65	180	64.1	281	7	ADB61480 Human Apo
66	180	64.1	281	7	ADB61482 Human Apo
67	180	64.1	281	7	ADB61484 Human Apo
68	180	64.1	281	7	ADB61478 Human Apo
69	180	64.1	281	7	ADB61481 Human Apo
70	180	64.1	281	7	ADB61487 Human Apo
71	180	64.1	281	7	ADB61485 Human Apo
72	180	64.1	281	7	ADB61490 Human Apo
73	180	64.1	281	7	ADB61477 Human Apo
74	180	64.1	281	7	ADB61479 Human Apo
75	180	64.1	281	7	ADB61486 Human Apo
76	180	64.1	281	7	ADB61488 Human Apo
77	180	64.1	281	7	ADB61483 Human Apo
78	180	64.1	281	7	ADB61489 Human Apo
79	177	63.0	267	6	ABU09032 Human tum
80	168	59.8	168	4	ABW76826 Human TRA
81	168	59.8	168	5	AAU9896 Human TNF
82	168	59.8	423	3	AB28693 FC-huAGP-
83	166	59.1	166	3	AAO8274 Amino aci
84	161	57.3	161	4	AAW71985 C-termina
85	161	57.3	161	6	ABR39855 TNF famil
86	161	57.3	161	7	ADC03335 Tumour ne
87	161	57.3	161	6	ABR84402 TRAIL ami
88	156	55.5	296	4	AB86309 Fusion co
89	141	50.2	246	5	AAU79598 Human TRA
90	139	49.5	139	2	AAO15118 Polypepti
91	123	43.8	270	6	ABR82204 Chimeric
92	107	38.1	113	5	AAU79600 Human TRA
93	105	37.4	188	5	AAU79599 Human TRA
94	103	36.7	121	3	ABG03752 Human sec
95	91	32.4	173	5	ABG72258 Partial h
96	90	32.0	98	5	AAU79595 Human TNF
97	90	32.0	101	2	AAW19790 Human apo
98	90	32.0	101	2	AAW56761 Human TRA

99 90 32.0 101 4 AAEL11032 Human TRA
100 90 32.0 101 6 ABU08559 Human TNF

ALIGNMENTS

RESULT 1
AAW19777
ID AAW19777 standard; protein; 281 AA.

AC AAW19777;

XX 22-SEP-1997 (first entry)

XX Novel cytokine Apo-2 ligand.

XX Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..281

FT Region /note= "Claim 4"

FT Protein /label= Cytoplasmic_region

FT Region /note= "Claim 3"

FT Region /label= Transmembrane_region

FT Protein /note= "Claim 2"

FT Region /label= Extracellular_region

FT Modified-site 109

FT /label= Glycosylation

FT /note= "putative N-linked glycosylation site"

FT Protein 114..281

FT /note= "Claim 1"

XX WO9725428-A1.

XX 17-JUL-1997.

XX 08-JAN-1997; 97WO-US000272.

XX 09-JAN-1996; 96US-00584031.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Chuntharapai A, Kim KJ;

XX WPI; 1997-372867/34.

XX N-PSDB; AAW72796.

XX Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce

XX apoptosis for the treatment of breast and colon cancer.

XX Claim 4; Fig 1a; 72pp; English.

XX A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian

XX cell apoptosis. It is believed to be a member of the tumour necrosis

XX factor cytokine family. Its amino acid sequence was deduced from a cDNA

XX clone (AAW72796) isolated from a human placental cDNA library. Apo-2

XX ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-

XX 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells

XX transformed or transfected with a vector contg. Apo-2 ligand nucleic

XX acid. They can be used to induce apoptosis in mammals and to treat

XX pathological conditions such as cancer (esp. breast or colon cancer) or

XX to raise antibodies useful in diagnostic assays

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSPPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSPPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKTSYDPDILLMKSARNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKTSYDPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 2

AAW27134

ID AAW27134 standard; protein; 281 AA.

AC AAW27134;

XX 02-APR-1998 (first entry)

XX Human Apoptosis inducing molecule-I (AIM-I).

XX Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;

XX tumour necrosis factor ligand superfamily; AIM-I altered expression;

XX neoplasia inhibition; anti-inflammatory agent.

XX Homo sapiens.

XX WO9733899-A1.

XX 18-SEP-1997.

XX 14-MAR-1996; 96WO-US003773.

XX 14-MAR-1996; 96WO-US003773.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM;

XX WPI; 1997-470807/43.

XX N-PSDB; AAT85210.

XX New isolated apoptosis inducing molecule-I - used to develop products for

XX the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft

XX versus host disease or inflammation.

XX Claim 2; Fig 1; 82pp; English.

XX The present sequence represents a human Apoptosis inducing molecule-I

XX (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand

XX superfamily. The products can be used in the diagnosis and treatment of

XX disorders related to under-expression, over-expression or altered

XX expression of AIM-I. AIM-I or agonists can be used for treating

XX autoimmune disorders including systemic lupus erythematosus,

XX immunoproliferative disease lymphadenopathy (lF),

XX angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,

XX diabetes, and multiple sclerosis, graft versus host disease, to inhibit

XX neoplasia such as tumour cell growth, to treat restenosis, to regulate

XX haematopoiesis in endothelial cell development, to stimulate peripheral

CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
 CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or
 CC osteoporosis, for preventing graft-host rejection, and as anti-
 CC inflammatory agents, for treating endotoxin shock or to prevent
 CC activation of HIV
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGGTCLVIVFTVLLQSLCAVATVYVFTNELKQMDKYSGGIACFLKE 60
 DB 1 MAMMEVQGGPSLGGTCLVIVFTVLLQSLCAVATVYVFTNELKQMDKYSGGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCQVQKQLRQLVRKMLIRTSSTISVQEKQNISPLVRERGPO 120
 DB 61 DDSYWDPNDEESMNSPCQVQKQLRQLVRKMLIRTSSTISVQEKQNISPLVRERGPO 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 QY 181 FYIYSQYFRFOEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCKDAEYGLY 240
 DB 181 FYIYSQYFRFOEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 3
 AAW19787
 ID AAW19787 standard; protein; 281 AA.
 XX
 AC AAW19787;
 XX
 DT 24-SEP-1997 (first entry)
 XX
 DE Human apoptosis inducer cytokine TRAIL.
 XX
 KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
 KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
 KW thrombotic microangioplasty; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..18
 FT Domain /label= Cytoplasmic_domain
 FT Domain 19..38
 FT Domain /label= Transmembrane_domain
 FT Domain 39..281
 FT Domain /label= Extracellular_domain
 FT /note= "contains a receptor-binding region"
 FT Cleavage-site 89..90
 FT /note= "potential KEX2 protease processing site"
 FT Modified-site 109..111
 FT /note= "potential N-glycosylation site"
 FT Cleavage-site 149..150
 FT /note= "potential KEX2 protease processing site"
 XX
 PN WO9701633-A1.
 XX
 XX 16-JAN-1997.
 XX
 XX 25-JUN-1996; 96WO-US010895.
 XX
 XX 29-JUN-1995; 95US-00496632.
 XX 01-NOV-1995; 95US-00548368.
 XX

PA (IMMV) IMMUNEX CORP.
 XX
 PI Wiley SR, Goodwin RG;
 XX
 DR WPI; 1997-118715/11.
 DR N-PSDB; AAT72847.
 XX

PT TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
 PT cells - useful for treating thrombotic microangiopathy, cancer and viral
 PT infection and for use in assays.
 XX
 XX Claim 10; Page 43-44; 52pp; English.

XX Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
 CC (AAW19787) is a novel cytokine that induces apoptosis of certain target
 CC cells, including cancer cells and virally infected cells. Its amino acid
 CC sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in
 CC vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
 CC polypeptides) can be expressed in host cells and used in the treatment of
 CC cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
 CC to raise antibodies that may be useful for treating thrombotic
 CC microangiopathies
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGGTCLVIVFTVLLQSLCAVATVYVFTNELKQMDKYSGGIACFLKE 60
 DB 1 MAMMEVQGGPSLGGTCLVIVFTVLLQSLCAVATVYVFTNELKQMDKYSGGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCQVQKQLRQLVRKMLIRTSSTISVQEKQNISPLVRERGPO 120
 DB 61 DDSYWDPNDEESMNSPCQVQKQLRQLVRKMLIRTSSTISVQEKQNISPLVRERGPO 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 QY 181 FYIYSQYFRFOEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCKDAEYGLY 240
 DB 181 FYIYSQYFRFOEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 4
 AAW76829
 ID AAW76829 standard; protein; 281 AA.
 XX
 AC AAW76829;
 XX

DT 25-JAN-1999 (first entry)
 XX
 DE Human TL2 protein.
 XX

XX TR6; tumour necrosis factor related receptor; human; treatment; stroke;
 XX inflammation; arthritis; septicemia; autoimmune disease; restenosis;
 XX transplant rejection; infection; ischaemia; brain injury; bone disease;
 XX acute respiratory disease syndrome; acquired autoimmune disease syndrome;
 KW AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF;
 KW TL2; tumour necrosis factor-related apoptosis-inducing ligand.
 XX

OS Homo sapiens.
 XX
 XX EP870827-A2.
 XX
 PD 14-OCT-1998.
 XX

```
PF 23-DEC-1997; 97EP-00310562.
XX
PR 14-MAR-1997; 97US-0041230P.
PR 09-MAY-1997; 97US-00853684.
PR 22-AUG-1997; 97US-00916625.
XX
PA (SMIX ) SMITHKLINE BEECHAM CORP.
XX
PI Deen KC, Young PR;
XX
XX WPI; 1998-523156/45.
XX N-PSDB; AAV63096.
XX
XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding
XX polypeptide, antibody, agonist, antagonist, etc.
XX
XX Disclosure; Page 32-33; 34pp; English.
XX
XX This sequence represents the human tumour necrosis factor (TNF)-related
XX receptor, TL2 (also known as tumour necrosis factor-related apoptosis-
XX inducing ligand, TRAIL). This protein is used in a method resulting in
XX the isolation of the novel human TNF related receptor, TR6. TR6
XX polypeptides and polynucleotides can be used in the treatment of chronic
XX and acute inflammation, arthritis, septicemia, autoimmune diseases (e.g.
XX inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
XX host disease, infection, stroke, ischaemia, acute respiratory disease
XX syndrome, restenosis, brain injury, (acquired autoimmune disease
XX syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative
XX disorders), atherosclerosis and Alzheimers disease
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 281; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-266;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
XX DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
XX
XX QY 61 DDSYWDPNDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
XX DB 61 DDSYWDPNDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
XX
XX QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
XX DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
XX
XX QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYVDPDILLMKSARNCSKDAEYGLY 240
XX DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYVDPDILLMKSARNCSKDAEYGLY 240
XX
XX QY 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281
XX DB 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281
XX
XX RESULT 5
XX AAW56760
XX ID AAW56760 standard; protein; 281 AA.
XX
XX AC AAW56760;
XX
XX DT 05-AUG-1998 (first entry)
XX
XX XX Human TRAIL polypeptide.
XX
XX XX Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
XX cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
XX
XX OS Homo sapiens.
XX
XX XX Key Location/Qualifiers
XX
```

```
FT Domain
FT FT /note= "N-terminal cytoplasmic domain"
FT Region 19..38
FT FT /note= "transmembrane region"
FT Domain 39..281
FT FT /note= "extracellular domain"
XX
XX US5763223-A.
XX PN
XX PD 09-JUN-1998.
XX
XX PF 25-JUN-1996; 96US-00670354.
XX
XX PR 29-JUN-1995; 95US-00496632.
XX PR 01-NOV-1995; 95US-00548368.
XX
XX PA (IMMV ) IMMUNEX CORP.
XX
XX XX Goodwin RG, Wiley SR;
XX PI
XX DR WPI; 1998-347322/30.
XX N-PSDB; AAV29518.
XX
XX DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful
XX for producing recombinant polypeptides for research and therapy of
XX leukaemia, lymphoma, melanoma and viral infections.
XX
XX PS Claim 1; Col 33-36; 28pp; English.
XX
XX CC This represents a human tumour necrosis factor related apoptosis ligand
XX (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce
XX apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful
XX for producing the recombinant TRAIL polypeptides, which may be useful in
XX studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
XX (e.g. to isolate antigens for vaccine development). The polypeptides can
XX be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
XX treatment of blood or bone-marrow), or to treat viral infections
XX
XX SQ Sequence 281 AA;
XX
XX Query Match 100.0%; Score 281; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-266;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
XX DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
XX
XX QY 61 DDSYWDPNDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
XX DB 61 DDSYWDPNDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
XX
XX QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
XX DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
XX
XX QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYVDPDILLMKSARNCSKDAEYGLY 240
XX DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYVDPDILLMKSARNCSKDAEYGLY 240
XX
XX QY 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281
XX DB 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281
XX
XX RESULT 6
XX AAW44354
XX ID AAW44354 standard; protein; 281 AA.
XX
XX AC AAW44354;
XX
XX DT 28-MAY-1998 (first entry)
XX
```

DE Human AGP-1.
 XX Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
 KW bone resorption; haematopoietic disease.
 XX Homo sapiens.
 XX WO9746686-A2.
 XX 11-DEC-1997.
 XX 06-JUN-1997; 97MO-US009895.
 XX 07-JUN-1996; 96US-00660562.
 XX (AMGE-) AMGEN INC.
 XX Johnson MJ, Simonet WS, Danilenko DM;
 XX WPI; 1998-042194/04.
 XX DR N-PSDB; AAV15295.
 XX Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -
 PT useful for treating inflammation, bone resorption and haematopoietic
 XX diseases.
 XX Claim 7; Page 36-37; 54pp; English.
 XX The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
 CC factor (TNF)-related protein, involved in inflammation, myelopoiesis and
 CC bone resorption. It has the same nucleic acid and amino acid (aa)
 CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
 CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
 CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
 CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
 CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or
 CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,
 CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat
 CC haematopoietic diseases associated with reduction in the number of bone
 CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
 CC by disease, injury or exposure to myelosuppressive agents. Host cells,
 CC transformed with expression vectors containing AGP-1 DNA, are used to
 CC produce recombinant AGP-1
 XX Sequence 281 AA;
 SQ Query Match 100.0%; Score 281; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMVEVQGPSLGGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMVEVQGPSLGGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGPO 120
 DB 61 DDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGPO 120
 QY 121 RVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 DB 121 RVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 QY 181 FYIYISQTYFRQBEIKENTKNDKQVQYIKYTSYDPDILLMKARNCSWKDAEYGLY 240
 DB 181 FYIYISQTYFRQBEIKENTKNDKQVQYIKYTSYDPDILLMKARNCSWKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 RESULT 7

AAV01517
 ID AAY01517 standard; peptide; 281 AA.
 XX AC AAY01517;
 XX DT 27-MAY-1999 (first entry)
 XX DE Protein associated with neurodegenerative and autoimmune diseases.
 XX KW Neurodegenerative disease; autoimmune disease; inflammatory disease;
 XX KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
 XX KW surface receptor; TRAIL protein.
 XX OS Homo sapiens.
 XX PN FR2766713-A1.
 XX PD 05-FEB-1999.
 XX PF 04-AUG-1997; 97FR-00010176.
 XX PR 04-AUG-1997; 97FR-00010176.
 XX PA (INMR) BIO MERIEUX.
 XX PI Rieger F, Belliveau JF, Perron H;
 XX WI 1999-156177/14.
 XX Use of polypeptide derived from TRAIL protein for diagnosis of
 FT degenerative disease - autoimmunity and inflammation, also useful in
 FT prevention or treatment, and similar use of corresponding ligand and
 FT nucleic acid.
 XX Claim 2; Page 13; 21pp; French.
 XX The specification describes the use a polypeptide corresponding to at
 CC least the primary sequence of part of the present sequence to produce a
 CC diagnostic, prophylactic or therapeutic composition useful in cases of
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
 CC be used in treatment of neurodegenerative disease, lupus erythematosus,
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
 CC nervous system cells, antigenic and specifically recognise the surface
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
 CC receptors, inhibiting formation of natural complex
 XX Sequence 281 AA;
 SQ Query Match 100.0%; Score 281; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMVEVQGPSLGGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMVEVQGPSLGGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGPO 120
 DB 61 DDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGPO 120
 QY 121 RVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 DB 121 RVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 QY 181 FYIYISQTYFRQBEIKENTKNDKQVQYIKYTSYDPDILLMKARNCSWKDAEYGLY 240
 DB 181 FYIYISQTYFRQBEIKENTKNDKQVQYIKYTSYDPDILLMKARNCSWKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 8
 AAY27012
 ID AAY27012 standard; protein; 281 AA.
 AC AAY27012;
 DT 24-SEP-1999 (first entry)
 XX Human Apo-2 ligand (Apo-2L) polypeptide.
 DE Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
 KW lupus; immune-mediated glomerular nephritis; human.
 XX Homo sapiens.
 OS
 XX WO9936535-A1.
 FN 22-JUL-1999.
 PD 15-JAN-1999; 99WO-US001039.
 PF 15-JAN-1998; 98US-00007886.
 PR 15-APR-1998; 98US-00060533.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;
 PI WPI; 1999-444397/37.
 DR N-PSDB; AAX86987.
 XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 PT in mammalian cancer cells.
 XX Claim 1; Fig 1A; 86pp; English.
 PS This sequence represents a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis
 XX Sequence 281 AA;
 SQ
 Query Match 100.0%; Score 281; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMVEVGGPSLGQTCVLIIVITVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60
 DB 1 MAMVEVGGPSLGQTCVLIIVITVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60
 QY 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 DB 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYYIYSQTYFRFQBEIKENTKNDKQMVYIKYTSYDPDILLMKSARNCSWSDAEYGLY 240
 DB 181 FYYIYSQTYFRFQBEIKENTKNDKQMVYIKYTSYDPDILLMKSARNCSWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
 RESULT 9
 AAY81956
 ID AAY81956 standard; protein; 281 AA.
 AC AAY81956;
 DT 10-JUL-2000 (first entry)
 XX Human Apo-2 ligand protein sequence.
 DE Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
 KW therapy; apoptosis; cancer.
 XX Homo sapiens.
 OS
 XX US6046048-A.
 FN 04-APR-2000.
 PD 08-JAN-1997; 97US-00780496.
 PF 09-JAN-1996; 96US-0009755P.
 PR (GETH) GENENTECH INC.
 PA Kim KJ, Ashkenazi AJ, Chuntharapai A;
 PI WPI; 2000-282690/24.
 DR N-PSDB; AAA07425.
 XX New isolated monoclonal antibodies having antigen specificity for Apo-2
 PT ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo
 PT -2 ligand serum, and for treating diseases associated with increased
 PT apoptosis.
 XX Claim 9; Fig 1a; 46pp; English.
 PS This sequence is the human Apo-2 ligand protein, which is recognised by
 CC monoclonal antibodies produced by the hybridoma cell lines of the
 CC invention. The hybridoma cell lines are deposited under the American Type
 CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
 CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
 CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
 CC tissues, or serum. The antibodies may also be employed as therapeutics.
 CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
 CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
 CC pathological conditions or diseases associated with increased apoptosis.
 CC They are also useful for the affinity purification of Apo-2 ligand from
 CC recombinant cell culture or natural sources. The Apo-2 ligand itself may
 CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells
 XX Sequence 281 AA;
 SQ
 Query Match 100.0%; Score 281; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMVEVGGPSLGQTCVLIIVITVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60
 DB 1 MAMVEVGGPSLGQTCVLIIVITVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60
 QY 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 DB 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYYIYSQTYFRFQBEIKENTKNDKQMVYIKYTSYDPDILLMKSARNCSWSDAEYGLY 240

Db 181 FYIYISQTYFRFOBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 10
AAB24038
ID AAB24038 standard; protein; 281 AA.
XX AC AAB24038;
XX WO200053750-A1.
XX 14-SEP-2000.
XX 02-DEC-1999; 99WO-US028551.
XX 08-MAR-1999; 99WO-US005028.
XX 01-SEP-1999; 99WO-US020111.
XX 29-OCT-1999; 99US-O162506P.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028634.
XX (GETH) GENENTECH INC.
XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
XX WPI; 2000-594320/56.
XX N-PSDB; AAC58120.
XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit
XX the growth of tumors in mammals, and to identify inhibitors of PRO
XX polypeptide activity or expression.
XX Claim 61; Fig 36; 226pp; English.
XX The present invention describes an antibody that binds to a human protein
XX (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
XX PRO1927; PRO3567; PRO1295; PRO1303; PRO1344; PRO4354; PRO4397;
XX PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
XX activity and can be used to diagnose tumours in mammals, by detecting
XX complex formation when the antibody is contacted with test cells.
XX Increased expression of genes encoding (I) can also be detected to
XX diagnose tumours. Agents which inhibit the activity of (I), especially
XX the antibodies, or an antisense oligonucleotide which hybridises to genes
XX encoding (I), can be used to inhibit tumour growth, preferably by
XX inducing cell death. Methods from the present invention can be used to
XX identify compounds which inhibit the biological activity of (I). AAC58019
XX to AAC58102 represent PCR primers and hybridisation probes used in
XX examples from the present invention for human PRO sequences. AAC58103 to
XX AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
XX protein sequences given in the exemplification of the present invention
XX Sequence 281 AA;
XX Query Match 100.0%; Score 281; DB 3; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-266;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLQGTCLVIVFTVLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEVGGPSLQGTCLVIVFTVLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRXWILRTSEETISTVQEKQOONISPLVRRGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRXWILRTSEETISTVQEKQOONISPLVRRGPQ 120
QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 180
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 180
QY 181 FYIYISQTYFRFOBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYISQTYFRFOBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 11
AAB08545
ID AAB08545 standard; protein; 281 AA.
XX AC AAB08545;
XX 20-DEC-2000 (first entry)
XX Amino acid sequence of a human TRAIL polypeptide.
XX Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;
XX TNF related apoptosis-inducing ligand; tumour cell;
XX TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;
XX non-small cell lung carcinoma.
XX Homo sapiens.
XX WO200048619-A1.
XX 24-AUG-2000.
XX 15-FEB-2000; 2000WO-US003891.
XX 16-FEB-1999; 99US-0120313P.
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX Rosen GD;
XX WPI; 2000-558253/51.
XX N-PSDB; AAA64325.
XX Killing of tumor cells, e.g. solid tumors or carcinoma, comprises
XX administration of synergistic combination of diterpenoid diepoxide and
XX tumor necrosis factor related apoptosis-inducing ligand.
XX Disclosure; Page 23-24; 29pp; English.
XX The present sequence represents a human TRAIL (tumour necrosis factor
XX (TNF) related apoptosis-inducing ligand) polypeptide. The specification
XX describes a method for enhanced killing of tumour cells. The method
XX comprises contacting a susceptible tumour cell with a synergistic mixture
XX of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined
XX dosage to kill at least 50 % of the cells. This mixture is synergistic,
XX and so is active at lower doses and against otherwise resistant cell
XX lines. The method is used for killing tumour cells, especially solid
XX tumours or carcinomas (especially mammary carcinoma or non-small cell
XX lung carcinoma)
XX Sequence 281 AA;
XX SQ

Query Match 100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVIFVTLVQLSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 Db |||||
 1 MAMMEVQGGPSLQGTCLVIFVTLVQLSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
 Db |||||
 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
 QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
 Db |||||
 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKARNCSWSDAEYGLY 240
 Db |||||
 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKARNCSWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db |||||
 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 12

AAB28691
 ID AAB28691 standard; protein; 281 AA.

XX AC AAB28691;

XX DT 14-FEB-2001 (first entry)

XX DE Human AGP-1.

XX KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
 KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
 KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
 KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
 KW transplant rejection; cardiovascular disease; arteriosclerosis.

XX OS Homo sapiens.

XX PN WO200063253-A1.

XX PD 26-OCT-2000.

XX PF 24-MAR-2000; 2000WO-US008004.

XX PR 16-APR-1999; 99US-00293245.

XX PA (AMGE-) AMGEN INC.

XX PI Hsu H, Meng S;

XX XX WPI; 2000-665240/64.

XX DR N-PSDE; AAC67831.

XX PT Fusion protein of AGP-1 protein and an Fc region, used to treat
 XX proliferative disorders, immune disorders, and virally-induced disorders.

XX PS Claim 3; Fig 2; 93pp; English.

XX CC The present sequence is human AGP-1, a type II transmembrane protein.
 CC Fusion proteins comprising an Fc immunoglobulin region fused to the N-
 CC terminal portion of the AGP-1 protein have been produced. The fusion
 CC proteins can be used to induce apoptosis in a tissue, and to treat
 CC proliferative disorders, immune disorders, or virally-induced disorders.
 CC The proliferative disorders include cancers, such as breast, prostate,
 CC lung or colon cancer. The viral infections include hepatitis, and
 CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
 CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
 CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion
 CC proteins have increased biological activity compared to the soluble AGP-1
 CC proteins used in prior art therapies

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVIFVTLVQLSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 Db |||||
 1 MAMMEVQGGPSLQGTCLVIFVTLVQLSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
 Db |||||
 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
 QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
 Db |||||
 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKARNCSWSDAEYGLY 240
 Db |||||
 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKARNCSWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db |||||
 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 13

AAB50977

ID AAB50977 standard; protein; 281 AA.

XX AC AAB50977;

XX DT 21-MAR-2001 (first entry)

XX DE Human PRO1096 protein.

XX KW Human; PRO; cytostatic; neutropic; neuroprotective; respiratory general;
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.

XX OS Homo sapiens.

XX PN WO200073348-A2.

XX PD 07-DEC-2000.

XX PF 30-MAY-2000; 2000WO-US014941.

XX PR 02-JUN-1999; 99WO-US012252.

XX PR 22-JUN-1999; 99US-0140650P.

XX PR 23-JUN-1999; 99US-0141037E.

XX PR 20-JUL-1999; 99US-0144758P.

XX PR 01-SEP-1999; 99WO-US020111.

XX PR 08-SEP-1999; 99WO-US020594.

XX PR 29-OCT-1999; 99US-0162506P.

XX PR 30-NOV-1999; 99WO-US028313.

XX PR 01-DEC-1999; 99WO-US028634.

XX PR 02-DEC-1999; 99WO-US028551.

XX PR 09-DEC-1999; 99US-0170262P.

XX PR 20-DEC-1999; 99WO-US030999.

XX PR 06-JAN-2000; 2000WO-US000376.

XX PR 11-FEB-2000; 2000WO-US003565.

XX PR 18-FEB-2000; 2000WO-US004341.

XX PR 18-FEB-2000; 2000WO-US004342.

XX PR 02-MAR-2000; 2000WO-US005841.

XX PR 03-MAR-2000; 2000US-0187202P.

XX PR 10-MAR-2000; 2000WO-US006319.

XX PR 15-MAR-2000; 2000WO-US006884.

XX PR 30-MAR-2000; 2000WO-US008439.

XX PR 17-MAY-2000; 2000WO-US013705.

XX

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PA (GETH ) GENENTECH INC.
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WL;
XX WPI; 2001-016509/02.
DR N-PSDB; AAC91579.
XX
XX Twenty eight nucleic acids encoding PRO polypeptides which are useful for
XX treating various tumors, e.g. breast cancer, and other inflammatory,
XX angiogenic and immunological disorders.
XX
XX Claim 31; Fig 54; 188pp; English.
XX
XX The present sequence is one of twenty eight novel PRO polypeptides. The
XX PRO polypeptides and their agonists, including antibodies, peptides, and
XX small molecule agonists, may be used to treat various tumors, e.g.,
XX cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
XX cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
XX central nervous system cancer, melanoma or leukaemia. They are also
XX useful for treating other disorders such as neuronal, glial, astrocytal,
XX hypothalamic and other glandular, macrophagal, epithelial, stromal and
XX blastocoeleic disorders, and inflammatory, angiogenic and immunological
XX disorders
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVTYVFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVTYVFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGPO 120
DB 61 DDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHDEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHDEASFFGAFLVG 281
RESULT 14
AAB67243
ID AAB67243 standard; protein; 281 AA.
XX
XX AAB67243;
XX
XX 18-APR-2001 (first entry)
XX
XX Human Apo2 ligand.
XX
XX Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
XX
XX Homo sapiens.
XX
XX WO2001008332-A1.
XX
XX 04-JAN-2001.
XX
XX 26-JUN-2000; 2000WO-US017579.
XX
XX 28-JUN-1999; 99US-0141342P.
XX

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XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
XX O'Connell M, Pai R, Shahrokh Z, Simmons L;
XX WPI; 2001-123012/13.
XX
XX Use of divalent metal ions for making Apo-2 ligand and in formulations
XX containing Apo-2 ligand for increasing yield and stability of ligand
XX trimers, useful for therapeutic applications.
XX
XX Claim 6; Fig 1; 60pp; English.
XX
XX The present invention relates to a formulation comprising Apo-2 ligand
XX and divalent metal ions. Apo-2 ligand and the formulation are useful for
XX treating cancers and viral infections. Addition of divalent metal ions
XX for making Apo-2 ligand and formulations containing Apo-2 ligand results
XX in increased yield and stability of Apo-2 ligand trimers
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVTYVFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVTYVFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGPO 120
DB 61 DDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHDEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHDEASFFGAFLVG 281
RESULT 15
AAE11031
ID AAE11031 standard; protein; 281 AA.
XX
XX AAE11031;
XX
XX 18-DEC-2001 (first entry)
XX
XX Human TNF related apoptosis inducing ligand (TRAIL) protein.
XX
XX Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
XX TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
XX human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
XX melanoma.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Domain 1..18 /label= N_terminal_cytoplasmic_domain
XX FT Region 19..38 /label= Transmembrane_region
XX FT Domain 39..281 /label= Extracellular_domain
XX
XX US6284236-B1.

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XX PD 04-SEP-2001.
 XX PF 26-MAY-1999; 99US-00320424.
 XX PR 29-JUN-1995; 95US-00496632.
 XX PR 01-NOV-1995; 95US-00548368.
 XX PR 25-JUN-1996; 96US-00670354.
 XX PR 26-MAR-1998; 98US-00048641.
 XX PR 10-NOV-1998; 98US-00190046.
 XX PA (IMNV) IMMUNEX CORP.
 XX PI Wiley SR, Goodwin RG;
 XX WPI; 2001-595463/67.
 XX DR N-PSDB; AAD18395.
 XX New tumor necrosis factor related apoptosis inducing ligand polypeptides
 PT for treating viral infections (e.g. bovine viral diarrhoea or human
 PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
 XX Claim 2; Col 45-48; 41pp; English.
 XX The invention relates to a cytokine designated as tumour necrosis factor
 CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
 CC of certain target cells, including cancer cells and virally infected
 CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
 CC treating viral infections (e.g. bovine viral diarrhoea or human
 CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
 CC melanoma), as a research reagent useful in studying apoptosis including
 CC the regulation of programmed cell death. TRAIL DNA sequences may be
 CC employed in developing a gene therapy approach to treating disorders
 CC mediated by defective or insufficient amounts of TRAIL, in the production
 CC of TRAIL polypeptides and as probes or primers in polymerase chain
 CC reactions (PCR). The present sequence is human TRAIL protein
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DSYWDPNDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 DB 61 DSYWDPNDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 16
 AAB48350
 ID AAB48350 standard; protein; 281 AA.
 XX
 AC AAB48350;
 XX
 XX 20-APR-2001 (first entry)
 XX Human TL2 polypeptide.

XX KW Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TL2;
 KW antiinflammatory; immunosuppressive; cerebroprotective; vasotropic;
 KW antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;
 KW neutropic; neuroprotective; antiarthritic; antirheumatic; antiischemic;
 XX gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.
 OS Homo sapiens.
 XX WO2000077191-A1.
 XX PD 21-DEC-2000.
 XX PF 12-JUN-2000; 2000WO-US016134.
 XX PR 15-JUN-1999; 99US-00333593.
 XX PA (SMIK) SMITHLINE BEECHAM CORP.
 XX PI Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;
 XX WPI; 2001-112223/12.
 XX DR N-PSDB; AAC84745.
 XX New tumor necrosis factor related receptor TR6 polynucleotides and
 PT polypeptides useful for e.g. for treating chronic and acute inflammation,
 PT arthritis, septicemia, autoimmune diseases, infection, cancer, bone
 PT diseases.
 XX Disclosure; Page 26; 47pp; English.
 XX The invention relates to a human tumour necrosis factor (TNF) related
 CC receptor, TR6. TR6 can be expressed by standard recombinant methodology.
 CC The TR6 polypeptides are useful for treating chronic and acute
 CC inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g.
 CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
 CC host disease, infection, stroke, ischaemia, acute respiratory disease
 CC syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,
 CC atherosclerosis, and Alzheimer's disease. These may also be used to
 CC inhibit production of TNF-alpha and eicosanoids, as research reagents and
 CC materials for discovering treatments and diagnostics to animal and human
 CC diseases. The polypeptides may further be used as immunogens to produce
 CC antibodies immunospecific for the TR6 polypeptides. The polynucleotides
 CC may also be used as hybridization probes for cDNA and genomic DNA for
 CC isolating full-length cDNAs and genomic clones encoding TR6 and of other
 CC genes having high sequence similarity to TR6 gene, and for chromosome
 CC identification. The present sequence represents a human TL2 polypeptide.
 CC TL2 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and is
 CC a ligand for the TL2 polypeptide
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DSYWDPNDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 DB 61 DSYWDPNDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

```

Db      241 SIYQGIPELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||
RESULT 17
ABB08133
ID ABB08133 standard; protein; 281 AA.
XX
AC ABB08133;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human TRAIL polypeptide.
XX
KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
KW fungicide; protoacide; virucide; anti-inflammatory; anti-HIV;
KW tuberculostatic; cytostatic; human; TRAIL.
XX
OS Homo sapiens.
XX
PN WO200236141-A2.
XX
PD 10-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US044834.
XX
PR 02-NOV-2000; 2000US-0245721P.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;
PI Thomas EK;
XX
DR WPI; 2002-500114/53.
XX
PT Treating an individual suffering from infection, e.g. inflammation,
PT chickenpox or AIDS, by administering a combination of dendritic cell
PT mobilization factor or maturation agent, T cell enhancing factor and
PT antigen-specific T cells.
XX
PS Disclosure; Page 40-42; 43pp; English.
XX
CC The invention relates to treating an individual at risk for or suffering
CC from infection with a pathogenic or opportunistic organism. The method
CC involves administering a combination of two to five agents comprising:
CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
CC agent; (c) dendritic cell activation factor; (d) T cell enhancing factor;
CC or (e) activated, antigen-specific T cells. The methods are useful for
CC treating an individual at risk for or suffering from infection with a
CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
CC T. cruzi, which causes Chaga's disease). The methods are especially
CC useful for treating an individual suffering from immunosuppression by
CC enhancing a lymphocyte-mediated immune response. In particular, the
CC method is useful for treating inflammations, chickenpox, oral or genital
CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T
CC cell leukemia or T cell lymphoma. The activated antigen-presenting
CC dendritic cells are useful as a vaccine adjuvant. The present sequence
CC represents a human TRAIL polypeptide fragment
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYSKGIACFLKE 60
Db 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYSKGIACFLKE 60
QY 61 DDSYWDPNDESMNSPCQVQKWLRLQLVRKMLRTSEETISTVQEKQNI SPLVRERGQP 120
Db 61 DDSYWDPNDESMNSPCQVQKWLRLQLVRKMLRTSEETISTVQEKQNI SPLVRERGQP 120

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QY 121 RVAAHITGRSNTLSPPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGRSNTLSPPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRPQBEIKENTKNDKQMVQYIYKYTSYDPDILLMSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRPQBEIKENTKNDKQMVQYIYKYTSYDPDILLMSARNSCWSKDAEYGLY 240
QY 241 SIYQGIPELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGIPELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

```

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RESULT 18
ABG31630
ID ABG31630 standard; protein; 281 AA.
XX
AC ABG31630;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human TRAIL protein.
XX
KW Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;
KW dendritic cell maturation agent; T cell enhancing factor; skin cancer;
KW antigen-specific T cell; prostate cancer; liver cancer; bone tumour;
KW brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;
KW actinic keratosis; dendritic cell maturation stimulator; cytostatic;
KW dendritic cell activator; T cell enhancer; human; TRAIL.
XX
OS Homo sapiens.
XX
PN WO200266044-A2.
XX
PD 29-AUG-2002.
XX
PF 23-OCT-2001; 2001WO-US046254.
XX
PR 24-OCT-2000; 2000US-0242868P.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;
XX WPI; 2002-674891/72.
XX
PT Treating an individual with tumors or cancers, e.g. liver cancer or brain
PT tumor, by administering a combination of dendritic cell populations, T
PT cell enhancing factors and activated, antigen-specific T cells.
XX
PS Disclosure; Page 41-43; 44pp; English.
XX
CC The present invention relates to a new method for treating a tumour-
CC bearing subject. The method involves administering a combination of 2 to
CC 5 agents comprising dendritic cell mobilisation factor, dendritic cell
CC maturation agent, tumour-killing agent, T cell enhancing factor or
CC activated, antigen-specific T cells. The method is useful for treating
CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver
CC cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or
CC cervical intraepithelial neoplasia. The present amino acid sequence
CC represents the human TRAIL protein that was used in the method of the
CC invention
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYSKGIACFLKE 60
Db 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYSKGIACFLKE 60

```

QY 61 DSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120
 Db 61 DSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNLHRLNGELVHEKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNLHRLNGELVHEKG 180
 QY 181 FYIYSQTYFRFOEBIKENTKNDKQVQIYKYTSYDPDPILLMKSAARNCSWKSDAEYGLY 240
 Db 181 FYIYSQTYFRFOEBIKENTKNDKQVQIYKYTSYDPDPILLMKSAARNCSWKSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 19

AAU75062
 ID AAU75062 standard; protein; 281 AA.
 AC AAU75062;
 XX
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
 XX
 KW TRAIL; TNF; apoptosis; tumour; death domain receptor ligand;
 KW diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1; carcinoma;
 KW mammary adenocarcinoma; non-small cell lung carcinoma;
 KW neurological malignancy; haematological malignancy; lichen planus;
 KW non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;
 KW malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
 KW non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
 KW T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
 KW discoid lupus erythematosus; human.
 XX
 OS Homo sapiens.
 XX
 XX
 PN US6329148-B1.
 XX
 PD 11-DEC-2001.
 XX
 PF 15-FEB-2000; 2000US-00505250.
 XX
 PR 16-FEB-1999; 99US-0120313P.
 PR 20-AUG-1999; 99US-0149989P.
 XX
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Rosen GD, Kao P;
 XX
 XX WPI; 2002-121125/16.
 DR N-PSDB; ABK13192.
 XX
 XX Use of a synergistic combination of death domain receptor ligands and
 PT diterpenoid triepoxides for killing of tumor cells.
 XX
 PS Disclosure; Col 17-20; 20pp; English.

XX
 CC This invention relates to a novel method for enhanced killing of tumour
 CC cells comprising contacting a tumour cell with a synergistic combination
 CC of a death domain receptor ligand and a diterpenoid triepoxide. This
 CC method has cytostatic activity and works by blocking TNF-alpha mediated
 CC induction of c-IAP2 and c-IAP1. The method of the invention may be used
 CC for treating tumours, particularly solid tumours, e.g. carcinoma, mammary
 CC adenocarcinoma and non-small cell lung carcinoma also neurological
 CC malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma,
 CC chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis
 CC fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-
 CC cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid
 CC lupus erythematosus, lichen planus. The combination may be administered

CC with other active agents, e.g. anti- metastatic, anti-tumour or anti-
 CC angiogenic agents. The potent synergy between the diterpenoids and the
 CC death domain ligands allows increased killing at equivalent or lower
 CC doses, and can sensitise otherwise resistant cells. This sequence
 CC represents the human TNF related apoptosis inducing ligand (TRAIL)
 CC protein sequence. TRAIL is a death domain receptor used in the used
 CC method of the invention in combination with diterpenoid triepoxides to
 CC kill tumours by induction of apoptosis

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVVYFTNELKQMDKYKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVVYFTNELKQMDKYKSGIACFLKE 60

QY 61 DSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120

Db 61 DSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNLHRLNGELVHEKG 180

Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNLHRLNGELVHEKG 180

QY 181 FYIYSQTYFRFOEBIKENTKNDKQVQIYKYTSYDPDPILLMKSAARNCSWKSDAEYGLY 240

Db 181 FYIYSQTYFRFOEBIKENTKNDKQVQIYKYTSYDPDPILLMKSAARNCSWKSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 20

AAU51077
 ID AAU51077 standard; protein; 281 AA.

XX
 AC AAU51077;

XX 30-MAY-2002 (first entry)

DT Human Apo-2 ligand (TRAIL).

DE Apo-2 ligand; Apo-2L; TRAIL; human; apoptosis; colorectal cancer; tumour;

XX antitumour; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX Protein 114..281

FT /note= "Apo-2L polypeptide used in method of Claim 18"

XX WO200209755-A2.

XX 07-FEB-2002.

XX 27-JUL-2001; 2001WO-US023691.

XX 27-JUL-2000; 2000US-0221256P.

XX (GETH) GENENTECH INC.

XX Escandon E, Fox JA, Kelley SK, Xiang H;

XX WPI; 2002-268997/31.

XX Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I
 PT inhibitor class, and Apo-2 ligand receptor agonist for enhancing
 PT apoptosis in mammalian cells, or for treating cancer in a mammal.
 XX

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PS Claim 18; Page 79-80; 84pp; English.
XX
CC The present sequence is that of human Apo-2L ligand (Apo-2L or TRAIL). The
CC invention relates to methods of inducing apoptosis in mammalian cells,
CC and especially to the use of Apo-2L receptor agonists and CPT-11 (a
CC chemotherapeutic agent of the topoisomerase I inhibitor class) to
CC synergistically induce apoptosis in mammalian cells, in particular
CC mammalian cancer cells, and especially colorectal cancer cells (claimed).
CC The cells may be in cell culture or in a mammal, e.g. a mammal suffering
CC from cancer or a condition in which induction of apoptosis in the cells
CC is desirable. A claimed method of treating cancer in a mammal comprises
CC administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is
CC administered about 6-72 hours prior to administration of the Apo-2L
CC receptor agonist. Preferred Apo-2L receptor agonists include Apo-2L
CC (especially amino acids 114-281 of the present sequence) and anti-DR4 or
CC anti-DR5 receptor antibodies. Exposure of the cancer cells to CPT-11 and
CC Apo-2L receptor agonist leads to upregulation of DR4 and DR5 receptors,
CC directing the cells towards an apoptotic pathway rather than cell cycle
CC arrest and possible DNA repair, thus providing enhanced antitumour
CC activity. An example illustrates the synergistic inhibition of tumour
CC growth by Apo-2L and CPT-11 in athymic nude mice injected s.c. with human
CC COLO205 colon carcinoma cells
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIVHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIVHEKG 180
QY 181 FYIYSOTYFRFQEEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
DB 181 FYIYSOTYFRFQEEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 21
ABP51954
ID ABP51954 standard; protein; 281 AA.
XX
AC ABP51954;
XX
DT 09-OCT-2002 (first entry)
XX
XX Human Apo-2 ligand protein sequence SEQ ID NO:4.
XX
XX Bacterial host; protease; degP; prc; spr; anti-VEGF antibody; antibody;
XX humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;
XX anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;
XX anti-CD11a; Fab; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab';
XX Homo sapiens.
XX
XX WO200248376-A2.
XX
XX 20-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US047591.
XX
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PR 14-DEC-2000; 2000US-0256162P.
XX (GETH) GENENTECH INC.
XX Chen CY;
XX
XX WPI; 2002-583522/62.
XX N-PSDB; ABQ73920.
XX
XX Novel Escherichia coli strain useful for producing polypeptide, deficient
XX in degP and prc encoding protease, and harboring mutant spr gene, product
XX of gene suppresses growth phenotypes of strains harboring prc mutants.
XX
XX Example 1; Fig 4; 63pp; English.
XX
XX The present invention describes an Escherichia coli strain (I) deficient
XX in chromosomal degP and prc encoding protease DegP and Prc, respectively,
XX and harbouring a mutant spr gene, the product of mutant spr gene
XX suppresses growth phenotypes exhibited by strains harbouring prc mutants.
XX (I) is useful for producing a polypeptide, by culturing (I) comprising
XX nucleic acid encoding the polypeptide, which is heterologous to the
XX strain, such that the nucleic acid is expressed, and recovering the
XX heterologous polypeptide from the strain. The heterologous polypeptide is
XX proteolytically sensitive. Culturing of (I) is performed in a fermentor
XX under conditions of high- or low-cell density fermentation. The
XX polypeptide is recovered from the periplasm or culture medium of the
XX strain. The polypeptide is an antibody (humanised or full-length
XX antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular
XX endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,
XX anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an
XX antibody fragment having a light chain (kappa light chain). The antibody
XX fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18
XX Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper
XX fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-
XX tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-
XX CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18
XX Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence
XX represents a human Apo-2 ligand amino acid sequence from the present
XX invention
SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIVHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIVHEKG 180
QY 181 FYIYSOTYFRFQEEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
DB 181 FYIYSOTYFRFQEEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 22
AAO19095
ID AAO19095 standard; protein; 281 AA.
XX
XX AAO19095;
XX

DT 22-NOV-2002 (first entry)
XX C neoformans antigen expressing dendritic cell related protein #4.
XX Human; fungicide; fungal infection; dendritic cell; antigen;
KW Cryptococcus neoformans; vaccine; immunostimulant.
XX Homo sapiens.
OS WO200266053-A2.
PN XX
PD 29-AUG-2002.
XX
PF 14-DEC-2001; 2001WO-US048288.
XX
PR 04-JAN-2001; 2001US-0259653P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Thomas EK;
XX
DR WPI; 2002-674896/72.
XX
XX Producing a population of activated, Cryptococcus neoformans antigen-presenting dendritic cells for preventing or treating C. neoformans infection comprises causing the obtained dendritic cells to present the antigen.
XX
PS Disclosure; Page 29-30; 32pp; English.
XX
XX The present invention relates to a method of producing a population of activated, Cryptococcus neoformans antigen-presenting dendritic cells, comprising causing the obtained dendritic cells to present the antigen and maturing the dendritic cells. The activated, C. neoformans antigen-expressing dendritic cells are useful for treating, or as vaccines or vaccine adjuvants against, C. neoformans infection, or for generating antigen-specific T cells. The present sequence is a human protein shown in the exemplification of the invention
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DSYNDPNDDEESNNSPCWQVKQLRVKMLRTSEETSTVQEKQNNISPLVRRGQ 120
Db 61 DSYNDPNDDEESNNSPCWQVKQLRVKMLRTSEETSTVQEKQNNISPLVRRGQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNHLRNGELVHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNHLRNGELVHEKG 180
QY 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSPDPILLMKARNCSWKDNEYGLY 240
Db 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSPDPILLMKARNCSWKDNEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAEFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAEFLVG 281
RESULT 23
AAU79593
ID AAU79593 standard; protein; 281 AA.
XX
AC AAU79593;
XX
DT 24-SEP-2002 (first entry)

XX Human TNF-related apoptosis inducing ligand (TRAIL) protein.
DE
XX Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
KW TRAIL; apoptosis; programmed cell death; differentiation; development;
KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
KW chromosome 3q26.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Domain 1..16
FT /note= "Cytoplasmic domain"
FT Domain 17..38
FT /note= "Transmembrane domain"
FT Domain 39..281
FT /note= "Extracellular domain"
FT Domain 118..256
FT /note= "TNF domain"
XX
XX US2002061525-A1.
PN
XX 23-MAY-2002.
PD
XX 16-MAY-2001; 2001US-00855544.
PF
XX 16-MAY-2000; 2000IL-00136156.
PR
XX (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
XX (SAVI/) SAVITZKY K.
PI Yelin R, Khoeravi R, Savitzky K;
XX WPI; 2002-479259/51.
DR
XX
XX New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.
PT
PT Disclosure; Fig 9; 29pp; English.
PS
XX The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumour necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms. Apoptosis is induced by certain cytokines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1 and DcR2, lacking the intracellular signalling death domain. TRAIL, induced by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity. Determining these factors could provide possible mechanisms for the induction of apoptosis of tumour cells. The splice variant polypeptides and polynucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of the TRAIL variant products. Diseases that may be treated include cancer, neurodegenerative

CC diseases, autoimmune diseases, diseases involved in the non-normal
 CC development of tissues and aging. TRAIL's gene is located on chromosome
 CC 3q26. The sequence presented is the wild-type human TNF-related apoptosis
 CC inducing ligand (TRAIL) protein
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGGIACFLKE 60
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGGIACFLKE 60
 QY 61 DDSYDNDPDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120
 Db 61 DDSYDNDPDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120
 QY 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 Db 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 QY 181 FYIYSQTYFRQBEIKENTKNDKQVQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 240
 Db 181 FYIYSQTYFRQBEIKENTKNDKQVQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 24

ABG73861
 ID ABG73861 standard; protein; 281 AA.

XX AC ABG73861;
 XX
 DT 03-APR-2003 (first entry)
 XX

DE Human Apo-2 ligand protein.

XX Human; Apo-2; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;
 KW nuclear factor-kappa B; NF-kappa B; Apo-2 ligand; AIDS;
 KW tumour necrosis factor receptor; acquired immunodeficiency syndrome;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW multiple sclerosis; retinitis pigmentosa; cerebellar degeneration;
 KW aplastic anaemia; myocardial infarction; stroke; reperfusion injury;
 KW toxin-induced liver disease; cancer; lupus; herpes virus infection.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 15..40
 FT Domain /note= "Transmembrane domain"
 FT Domain 41..281
 FT Modified-site 109
 FT /note= "Extracellular domain"
 FT /note= "N-glycosylated"

XX US6462176-B1.

XX 08-OCT-2002.

XX 11-SEP-1997; 97US-00928069.

XX 23-SEP-1996; 96US-0026943P.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ;

XX WPI; 2003-173840/17.

XX Human; Apo-2 ligand; apoptosis; gene therapy; inflammation; cancer;

DR N-PSDB; ABX15469.

XX Novel isolated Apo-3 polypeptide useful for inducing apoptosis in
 PT mammalian cells, for generating antibodies, in affinity purification
 PT techniques, and in competitive-type receptor binding assays.

XX Example 4; Fig 4; 52pp; English.

XX The invention relates to an Apo-3 polypeptide having an extracellular
 CC domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide
 CC has been found to scintillate or induce apoptotic activity in mammalian
 CC cells. Human Apo-3 exhibits similarities to the tumour necrosis factor
 CC receptor (TNFR) family of polypeptides. The invention also relates to a
 CC chimeric molecule comprising an extracellular domain sequence comprising
 CC residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The
 CC Apo-3 polypeptide is useful therapeutically to induce apoptosis in
 CC mammalian cells. Decreased levels of apoptosis has been associated with
 CC conditions such as cancer, lupus, and herpes virus infection. Increased
 CC levels of apoptosis are associated with diseases such as acquired
 CC immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's
 CC disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis
 CC pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial
 CC infarction, stroke, reperfusion injury, and toxin-induced liver disease.
 CC The Apo-3 polypeptide is also useful in non-therapeutic applications such
 CC as in quantitative diagnostic assays as a control against which samples
 CC containing unknown quantities of Apo-3 may be prepared, in generating
 CC antibodies, as standards in assays for Apo-3, in affinity purification
 CC techniques, and in competitive-type receptor binding assays. The chimeric
 CC molecule is useful therapeutically to inhibit apoptosis or nuclear factor
 CC kappa B (NF-kappa B) induction, or as an immunogen for producing anti-
 CC Apo-3 antibodies. The present sequence represents polypeptide sequence of
 CC the human Apo-2 ligand protein which is also reported to be involved in
 CC apoptotic cell death. In the current invention the apoptotic activity of
 CC the Apo-2 ligand protein was measured on human lymphoid cells

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGGIACFLKE 60

QY 61 DDSYDNDPDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120

Db 61 DDSYDNDPDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120

QY 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Db 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

QY 181 FYIYSQTYFRQBEIKENTKNDKQVQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 240

Db 181 FYIYSQTYFRQBEIKENTKNDKQVQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 25

ABU10205

ID ABU10205 standard; protein; 281 AA.

XX AC ABU10205;

XX 11-AUG-2003 (first entry)

XX Human Apo-2 ligand.

KW neurodegenerative disease; immunosuppressive; tissue typing.

XX Homo sapiens.

XX US2003004313-A1.

XX 02-JAN-2003.

XX 28-MAR-2002; 2002US-00112193.

XX 23-SEP-1996; 96US-0026943P.

XX 11-SEP-1997; 97US-00928069.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ;

XX WPI; 2003-438872/A1.

XX N-FSDB; ACA61636.

XX New isolated Apo-3 polypeptides, useful for stimulating or inducing
PT apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo
PT or ex vivo gene therapy techniques.

XX Example 4; Fig 4; 50pp; English.

XX The invention relates to an isolated Apo-3 polypeptide. The Apo-3
CC polypeptides are useful for stimulating or inducing apoptotic activity in
CC mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy
CC techniques. The Apo-3 chimeric molecules are useful for inhibiting
CC apoptosis, or as immunogens used in generating antibodies. The
CC antagonistic antibodies may be used to block excessive apoptosis, for
CC instance in neurodegenerative disease, or to block potential autoimmune/
CC inflammatory effects of Apo-3 resulting from NF-kappaB activation. The
CC nucleic acid sequences are useful as diagnostics for tissue-specific
CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or
CC knockout animals. The transgenic or knockout animals are useful in
CC developing and screening of therapeutically useful reagents. The present
CC sequence represents the amino acid sequence of human Apo-2 ligand
XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEYQGGPSLGQTCVLIVIFTLVLSQSLCVAVTVYFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEYQGGPSLGQTCVLIVIFTLVLSQSLCVAVTVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DSYWDNDPDEESMNSPCWQVKQLRQLVKRMILRTSEETISTVQEKQQNISPLVREGRGQ 120

Db 61 DSYWDNDPDEESMNSPCWQVKQLRQLVKRMILRTSEETISTVQEKQQNISPLVREGRGQ 120

QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWSSRSGHSLNHLNGLVHEKG 180

Db 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWSSRSGHSLNHLNGLVHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTDKQWQVIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240

Db 181 FYIYSQTYFRFQEEIKENTDKQWQVIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 26

ABU71443

ID ABU71443 standard; protein; 281 AA.

XX ABU71443;

AC ABU71443;

XX

DT 09-JUN-2003 (first entry)

XX Human neoplasia inhibiting PRO polypeptide PRO1096.

XX Human; tumour; cancer; neoplasia; liver cancer; sarcoma; breast cancer;
KW ovarian cancer; renal cancer; colorectal cancer; melanoma;
KW uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
KW gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;
KW central nervous system cancer; hepatic carcinoma; glioblastoma;
KW neuronal disorder; glial disorder; astrocytal disorder;
KW hypothalamic disorder; glandular disorder; macropthalgal disorder;
KW epithelial disorder; stromal disorder; blastocoelec disorder;
KW inflammatory disorder; angiogenic disorder; immunologic disorder.

XX Homo sapiens.

XX US2002192209-A1.

XX 19-DEC-2002.

XX 30-NOV-2001; 2001US-00001054.

XX 17-SEP-1997; 97US-0059114P.

XX 27-MAR-1998; 98US-0073689P.

XX 30-MAR-1998; 98US-0079920P.

XX 24-APR-1998; 98US-0082999P.

XX 29-APR-1998; 98US-0083545P.

XX 12-MAY-1998; 98US-0085149P.

XX 02-JUN-1998; 98US-0087607P.

XX 11-JUN-1998; 98US-0088588P.

XX 25-JUN-1998; 98US-0090691P.

XX 17-AUG-1998; 98US-0096891P.

XX 10-SEP-1998; 98US-0099803P.

XX 10-SEP-1998; 98US-0100263P.

XX 15-SEP-1998; 98US-0100390P.

XX 23-SEP-1998; 98US-0101476P.

XX 10-NOV-1998; 98US-0107783P.

XX 18-NOV-1998; 98US-0108849P.

XX 19-NOV-1998; 98US-01180997.

XX 15-DEC-1998; 98US-0112420P.

XX 22-DEC-1998; 98US-00218517.

XX 22-DEC-1998; 98US-0113296P.

XX 05-JAN-1999; 99WO-US000106.

XX 12-JAN-1999; 99US-0115554P.

XX 12-JAN-1999; 99US-0115558P.

XX 20-JAN-1999; 99US-0116533P.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1999; 99US-0123618P.

XX 12-APR-1999; 99US-00284291.

XX 20-APR-1999; 99WO-US008615.

XX 27-APR-1999; 99US-0131294P.

XX 02-JUN-1999; 99WO-US012952.

XX 22-JUN-1999; 99US-0140650P.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 25-AUG-1999; 99US-00380137.

XX 25-AUG-1999; 99US-00380138.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 09-SEP-1999; 99US-00380913.

XX 18-OCT-1999; 99US-00403297.

XX 29-OCT-1999; 99US-0162506P.

XX 10-NOV-1999; 99US-00423741.

XX 01-DEC-1999; 99WO-US028313.

XX 02-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028851.

XX 16-DEC-1999; 99US-0170262P.

XX 20-DEC-1999; 99WO-US030095.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
02-MAR-2000; 2000WO-US005841.
03-MAR-2000; 2000US-0187202P.
15-MAR-2000; 2000WO-US006884.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
08-NOV-2000; 2000US-00709238.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006566.
09-MAR-2001; 2001US-00802706.
25-MAY-2001; 2001US-00866034.
01-JUN-2001; 2001WO-US017092.
01-JUN-2001; 2001US-00872034.
01-JUN-2001; 2001US-00872035.
01-JUN-2001; 2001WO-US017800.
14-JUN-2001; 2001US-00882836.
20-JUN-2001; 2001WO-US019892.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
30-JUL-2001; 2001US-00918585.
06-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-00927796.
13-AUG-2001; 2001US-00929404.
28-AUG-2001; 2001WO-US0941992.
29-AUG-2001; 2001WO-US027099.
04-SEP-2001; 2001US-00946374.
(GETH) GENENTECH INC.
Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC,
Shelton DL, Smith V, Watanabe CK, Wood WI;
WPI: 2003-328851/06.
N-PSDB; ACA58016.
Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
treating tumor, preferably cancer, or for treating neuronal, glial,
hypothalamic, stromal, inflammatory, angiogenic and immunologic
disorders.
Claim 32; Fig 54; 186pp; English.
The invention relates to an isolated secreted and transmembrane
polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
associated signal peptide or PRO polypeptide extracellular domain with or
without its associated signal peptide. The PRO polypeptide or an antibody
binding to it is useful for inhibiting the growth of a tumor cell. A
composition containing a PRO polypeptide is useful for inhibiting
neoplastic cell growth or for treating a tumor, preferably cancer (such
as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
bladder, gastric, pancreatic, vulval, thyroid, central nervous system
cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
agonists. The PRO polypeptide or an antibody binding to it is useful in
the preparation of a medicament for treating a condition which is
responsive to the PRO polypeptide or an antibody binding to it. The PRO
polypeptide or an antibody binding to it is also useful for treating
neuronal, glial, astrocytic, hypothalamic, glandular, macrophagal,
epithelial, stromal, blastocoeic, inflammatory, angiogenic and
immunologic disorders. The present sequence represents the amino acid
sequence of a PRO polypeptide of the invention
Sequence 281 AA;
Query Match 100.0%; Score 281; DB 6; Length 281;
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
02-MAR-2000; 2000WO-US005841.
03-MAR-2000; 2000US-0187202P.
15-MAR-2000; 2000WO-US006884.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
08-NOV-2000; 2000US-00709238.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006566.
09-MAR-2001; 2001US-00802706.
25-MAY-2001; 2001US-00866034.
01-JUN-2001; 2001WO-US017092.
01-JUN-2001; 2001US-00872034.
01-JUN-2001; 2001US-00872035.
01-JUN-2001; 2001WO-US017800.
14-JUN-2001; 2001US-00882836.
20-JUN-2001; 2001WO-US019892.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
30-JUL-2001; 2001US-00918585.
06-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-00927796.
13-AUG-2001; 2001US-00929404.
28-AUG-2001; 2001WO-US0941992.
29-AUG-2001; 2001WO-US027099.
04-SEP-2001; 2001US-00946374.
(GETH) GENENTECH INC.
Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC,
Shelton DL, Smith V, Watanabe CK, Wood WI;
WPI: 2003-328851/06.
N-PSDB; ACA58016.
Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
treating tumor, preferably cancer, or for treating neuronal, glial,
hypothalamic, stromal, inflammatory, angiogenic and immunologic
disorders.
Claim 32; Fig 54; 186pp; English.
The invention relates to an isolated secreted and transmembrane
polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
associated signal peptide or PRO polypeptide extracellular domain with or
without its associated signal peptide. The PRO polypeptide or an antibody
binding to it is useful for inhibiting the growth of a tumor cell. A
composition containing a PRO polypeptide is useful for inhibiting
neoplastic cell growth or for treating a tumor, preferably cancer (such
as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
bladder, gastric, pancreatic, vulval, thyroid, central nervous system
cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
agonists. The PRO polypeptide or an antibody binding to it is useful in
the preparation of a medicament for treating a condition which is
responsive to the PRO polypeptide or an antibody binding to it. The PRO
polypeptide or an antibody binding to it is also useful for treating
neuronal, glial, astrocytic, hypothalamic, glandular, macrophagal,
epithelial, stromal, blastocoeic, inflammatory, angiogenic and
immunologic disorders. The present sequence represents the amino acid
sequence of a PRO polypeptide of the invention
Sequence 281 AA;
Query Match 100.0%; Score 281; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNKLQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNKLQMDKYSKSGIACFLKE 60
Qy 61 DDSYWDNDDEESMNSPCWQVKKQLRLVVRKMLRTSEETISTVOEKQONISPLVREGPQ 120
Db 61 DDSYWDNDDEESMNSPCWQVKKQLRLVVRKMLRTSEETISTVOEKQONISPLVREGPQ 120
Qy 121 RVAAHITGRSGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
Db 121 RVAAHITGRSGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYVDPDILLMKSARNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYVDPDILLMKSARNSCWSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 27
ABG72738
ID ABG72738 standard; protein; 281 AA.
XX AC ABG72738;
XX DT 17-FEB-2003 (first entry)
XX DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.
XX KW Human; allergic disease; allergy; TNF; TRAIL; diagnosis;
XX KW tumour necrosis factor-related apoptosis inducing ligand;
XX KW atopic skin inflammation.
XX OS Homo sapiens.
XX PN WO200283946-A1.
XX PD 24-OCT-2002.
XX PF 01-MAR-2002; 2002WO-JP001914.
XX PR 06-APR-2001; 2001JP-00108631.
XX PA (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN AGENCY NATION.
XX PI Sugita Y, Heishi M, Kagaya S, Gunji S, Tsujimoto G;
XX WI; 2003-093037/08.
XX DR N-PSDB; ABX13715.
XX PT Measurement of the expression level of TNF related apoptosis inducing
XX PT ligand gene for diagnosis and examination of allergic disease and
XX PT screening agents for allergic disease treatment.
XX PS Disclosure; Page 51-52; 58pp; Japanese.
XX CC The invention discloses a method for examining allergic diseases, which
XX CC comprises measuring the expression level of tumour necrosis factor (TNF)-
XX CC related apoptosis inducing ligand (TRAIL) gene in a specimen from the
XX CC patient and comparing this level with the level in healthy persons. TRAIL
XX CC gene expression is decreased in patients. The nucleic acids and
XX CC polypeptide can be used to screen for agents for the treatment of
XX CC allergic diseases, possibly using a transgenic rodent as a model animal
XX CC for the disease, with effectiveness determined by changes in expression
XX CC levels or protein activity. The method is useful for the diagnosis,
XX CC examination, prevention and treatment of allergic diseases, including
XX CC atopic skin inflammation. The sequence presented is the human TRAIL

CC protein
 XX Sequence 281 AA;
 SQ

Query Match
 Best Local Similarity 100.0%; Score 281; DB 6; Length 281;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60

QY 61 DSYWDPNDEESMNSPCWQKWLRLVRKMLRTSEETISTVQKQNMISPLVRGPQ 120
 DB 61 DSYWDPNDEESMNSPCWQKWLRLVRKMLRTSEETISTVQKQNMISPLVRGPQ 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 28
 AAO29543
 ID AAO29543 standard; protein; 281 AA.
 AC AAO29543;
 DT 27-AUG-2003 (first entry)
 DE Human TRAIL protein.
 XX

Human; TNF-related apoptosis-inducing ligand; Kaposi's sarcoma; cancer; hyperproliferative disorder; rheumatoid arthritis; Parkinson's disease; neurodegenerative disorder; Alzheimer's disease; Hashimoto's disease; allergic disorder; acquired immune deficiency syndrome; ocular disorder; myasthenia gravis; autoimmune disorder; Huntington's disease; vaccine; septic shock; multiple sclerosis; inflammatory disorder; liver injury; infectious diseases; myelodysplastic syndrome; cardiovascular disorder; graft-versus-host disease; toxin-induced liver disease; cachexia; AIDS; cerebrovascular disorder; thrombotic microangiopathy; aplastic anaemia; ischaemic injury; anorexia; diabetes; ulcerative colitis; psoriasis; asthma; AIDS; therapy; TRAIL receptor; TRAIL-R; AIM-I.

OS Homo sapiens.
 XX
 PN WO2003042367-A2.
 XX
 PD 22-MAY-2003.
 XX
 PF 13-NOV-2002; 2002WO-US036431.
 PR 14-NOV-2001; 2001US-0331309P.
 PR 07-MAY-2002; 2002US-0377973P.
 PR 15-AUG-2002; 2002US-0403376P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Salcedo T, Roschke V, Ruben SM, Rosen CA;
 XX
 DR WPI; 2003-449572/42.
 XX

Novel antibody against TNF-related apoptosis inducing ligand, useful for preventing, treating and ameliorating cancers and other hyperproliferative disorders, binds immunospecifically to TRAIL receptor 4 polypeptide.

XX Example 2; Page 392-393; 405pp; English.
 PS
 XX

The invention relates to antibodies that immunospecifically bind to tumour necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptors (TRAIL-R). Antibodies of the invention are useful for treating, preventing or ameliorating cancer (e.g. cancers of pancreas, uterine, breast, colon, lung and gastrointestinal and Kaposi's sarcoma) and other hyperproliferative disorders, neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease and Huntington's disease), autoimmune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis, myasthenia gravis, Hashimoto's disease and immunodeficiency syndrome), inflammatory disorders (e.g. asthma, allergic disorders and rheumatoid arthritis), infectious diseases (e.g. acquired immune deficiency syndrome; AIDS, herpes viral infections and other viral infections), myelodysplastic syndromes (e.g. aplastic anaemia), graft-versus-host disease, ischaemic injury, liver injury, toxin-induced liver disease, septic shock, cachexia, anorexia and proliferative disorders. Antibodies of the invention are also useful for treating cardiovascular disorders, cerebrovascular disorders, thrombotic microangiopathies, diabetes, ocular disorders associated with neovascularisation, psoriasis, and ulcerative colitis and for wound healing. The invention is also used to prepare vaccines. The present sequence is human TRAIL protein also known as AIM-I

XX Sequence 281 AA;
 SQ

Query Match
 Best Local Similarity 100.0%; Score 281; DB 6; Length 281;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60

QY 61 DSYWDPNDEESMNSPCWQKWLRLVRKMLRTSEETISTVQKQNMISPLVRGPQ 120
 DB 61 DSYWDPNDEESMNSPCWQKWLRLVRKMLRTSEETISTVQKQNMISPLVRGPQ 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 29
 ABU08558
 ID ABU08558 standard; protein; 281 AA.
 XX
 AC ABU08558;
 XX
 DT 05-JUN-2003 (first entry)
 DE Human TNF Related Apoptosis Inducing Ligand, TRAIL.
 XX

Human; TNF related apoptosis inducing ligand; TRAIL; tumour necrosis factor; apoptosis; haemostatic; immunosuppressive; anti-inflammatory; dermatological; thrombotic microangiopathy; thrombotic thrombocytopenic purpura; TTP; HUS; SLE; clotting disorder; adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS; systemic lupus erythematosus.

XX Homo sapiens.
 OS
 XX
 PN Key Location/Qualifiers
 FH Region 39..124
 FT

Db 61 DSYWDPNDESMNSPCQVQKWLRLVVKMILRTSEETISTVQKQKQNSPLVRERGQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHKG 180
 Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHKG 180
 QY 181 FYIYSQTYFRQBEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRQBEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 RESULT 31
 ID ABG71905 standard; protein; 281 AA.
 AC ABG71905;
 XX
 DT 20-JAN-2003 (first entry)
 XX
 DE Human TRAIL receptor-associated protein.
 XX
 KW Human; TRAIL receptor; tumour necrosis factor; TNF;
 KW light chain variable region TNF-related apoptosis-inducing ligand;
 KW antibody; VH; VL; cancer; heavy chain variable region; TR4; TR5; TR7;
 KW TR10; apoptosis; hyperproliferative disorder; hybridoma cell line;
 KW Kaposi's sarcoma; graft-versus-host disease; GVHD; infectious disease;
 KW AIDS; acquired immunodeficiency syndrome; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; autoimmune disorder;
 KW multiple sclerosis; Behcet's disease; lupus erythematosus;
 KW inflammatory disease; rheumatoid arthritis; psoriasis; wound healing;
 KW cardiovascular disorder; angiogenesis; immune response;
 KW chemotherapeutic agent.
 XX
 KW Homo sapiens.
 OS
 PN WC200279377-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 07-NOV-2001; 2001WO-US042996.
 XX
 PR 08-NOV-2000; 2000US-0246612P.
 PR 16-NOV-2000; 2000US-0248847P.
 PR 27-NOV-2000; 2000US-0252904P.
 PR 04-JUN-2001; 2001US-0295018P.
 PR 09-OCT-2001; 2001US-0327359P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Salcedo T, Roschke V, Ruben SM, Rosen CA;
 XX
 DR WPI; 2003-040669/03.
 XX
 PT Novel antibody for treating, or preventing disease or disorder, comprises
 PT amino acid sequence having identity to other amino acid sequence of
 PT either variable heavy/light chain-complementarity determining regions.
 XX
 PS Disclosure; Page 366; 375pp; English.
 XX
 CC The invention relates to an isolated antibody comprising a first amino
 CC acid sequence having 95 % identity to a second amino acid sequence of
 CC either variable heavy chain or light chain-complementarity determining
 CC regions (VHCDRI)/VLCDR2 or VHCDR3/VLCDR3 appearing as
 CC ABG71906-ABG71911 being specific for human TRAIL receptors 1-4 (TNF
 CC (tumour necrosis factor)-related apoptosis-inducing ligand receptor, also
 CC known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that
 CC produces the antibody, an antibody that binds the same epitope on a TR4
 CC polypeptide as the antibodies detailed above, detecting expression of a
 CC TR4 polypeptide(or detecting, diagnosing, prognosing or monitoring

CC cancers, and other hyperproliferative disorders) using the antibodies, a
 CC hybridoma cell line selected from the hybridoma cell lines contained in
 CC ATCC Deposit No. PTA-3149, PTA-2687, PTA-3369, PTA-2730, PTA-2729, PTA-
 CC 2728, PTA-3368, and PTA-2731 and the antibodies expressed by these
 CC hybridoma cell lines. The antibodies of the invention are useful for
 CC diagnosing or treating a disease or disorder associated with increased or
 CC decreased apoptosis, e.g. cancer (such as colon, breast, uterine,
 CC pancreatic, lung, gastrointestinal, and Kaposi's sarcoma), graft-versus-
 CC host disease (GVHD), infectious disease, acquired immunodeficiency
 CC syndrome (AIDS), or neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disease), autoimmune disorders like multiple
 CC sclerosis, Behcet's disease, lupus erythematosus, inflammatory diseases
 CC such as rheumatoid arthritis, and psoriasis, cardiovascular disorders, in
 CC promoting angiogenesis, wound healing, and in regulating immune response.
 CC Many other diseases and disorders are listed in the specification. The
 CC antibody is administered in combination with a chemotherapeutic agent
 CC selected from irinotecan, paclitaxel (TAXOL (RPM)), and gemcitabine. The
 CC antibody is useful as a diagnostic tool to monitor the expression of
 CC TRAIL receptor expression on cells, to detect, purify, and target the
 CC polypeptides, and in immunoassays for qualitatively and quantitatively
 CC measuring levels of TRAIL receptor polypeptides. The present sequence is
 CC a human TRAIL receptor associated protein. Note: The present sequence is
 CC included in the sequence listing but is not referred to anywhere else in
 CC the specification
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYKSGIACFLKE 60
 Db 1 MANMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYKSGIACFLKE 60
 QY 61 DSYWDPNDESMNSPCQVQKWLRLVVKMILRTSEETISTVQKQKQNSPLVRERGQ 120
 Db 61 DSYWDPNDESMNSPCQVQKWLRLVVKMILRTSEETISTVQKQKQNSPLVRERGQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHKG 180
 Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHKG 180
 QY 181 FYIYSQTYFRQBEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRQBEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 RESULT 32
 ID ABP60546 standard; protein; 281 AA.
 XX
 AC ABP60546;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE Human tumour necrosis factor TRAIL.
 XX
 KW APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
 KW dermatological; immunosuppressive; antitumour; antineoplastic;
 KW antithratic; cytostatic; antianaemic; antiallergic; antidiabetic;
 KW neuroprotective; ophthalmological; tuberculostatic; antidiabetic;
 KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
 KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
 KW inflammatory disorder; proliferative disorder; single chain antibody;
 XX
 OS Homo sapiens.

PN WO200294192-A2.
 XX 28-NOV-2002.
 XX 22-MAY-2002; 2002WO-US016106.
 XX 24-MAY-2001; 2001US-0293100P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM;
 XX WPI; 2003-156740/15.
 XX Novel isolated antibody that immunospecifically binds tumor necrosis
 XX factor delta, useful for treating, preventing or ameliorating Non-
 XX Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
 XX syndrome.
 XX
 XX Disclosure; Page 216-217; 225pp; English.
 XX The invention relates to a novel antibody or its fragment, which
 XX immunospecifically binds tumor necrosis factor Delta (TNF-delta/APRIL).
 XX The antibody of the invention has dermatological, immunosuppressive,
 XX antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,
 XX antiallergic, antiaethmatic, neuroprotective, ophthalmological,
 XX tuberculostatic, antidiabetic, antipsoriatic, anti-HIV,
 XX antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
 XX The antibody or its fragment are useful for treating, preventing or
 XX ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
 XX human, disease or disorder such as autoimmune disease, and graft versus
 XX host disease (GVHD). The autoimmune disease is systemic lupus
 XX erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
 XX is useful for detecting, diagnosing, prognosing, treating, preventing or
 XX ameliorating a disease or disorder associated with aberrant APRIL or
 XX APRIL receptor expression or aberrant function of APRIL or APRIL
 XX receptor. The disease or disorders includes autoimmune and inflammatory
 XX disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
 XX asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
 XX uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
 XX system, particularly B cell cancers, immune disorders such as myasthenia
 XX gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
 XX infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 XX proliferative disorders (e.g. leukemia). The present sequence represents
 XX the tumour necrosis factor TRAIL
 XX
 XX Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMVEVGGPSLGTCLVIFVFTVLLQSLQVAVTVYFTNKLQMDKYSKSGIACFLKE 60
 Db 1 MAMVEVGGPSLGTCLVIFVFTVLLQSLQVAVTVYFTNKLQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDNDSESNMSPCWQVKWQLRQLVRKMLTSETISTVQEKQNIISPLVRGPQ 120
 Db 61 DDSYWDNDSESNMSPCWQVKWQLRQLVRKMLTSETISTVQEKQNIISPLVRGPQ 120
 QY 121 RVAHHITGRSNTLSSPKNEKALGRKINSWESSRSGHFSNLHLRNGELVTHEKG 180
 Db 121 RVAHHITGRSNTLSSPKNEKALGRKINSWESSRSGHFSNLHLRNGELVTHEKG 180
 QY 181 FYYTSYTFRFBQEIKNKNDKQMVQYIKYKTSYDPDILLMKSARNSCWSKDAEYGLY 240
 Db 181 FYYTSYTFRFBQEIKNKNDKQMVQYIKYKTSYDPDILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 33
 AAE36258
 ID AAE36258 standard; protein; 281 AA.
 AC AAE36258;
 XX 26-JUN-2003 (first entry)
 XX Human TR4 ligand, TRAIL protein.
 XX
 XX TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;
 XX hyperproliferative disorder; neurodegenerative disorder; immune disorder;
 XX Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;
 XX retinitis pigmentosa; Parkinson's disease; Hashimoto's thyroiditis;
 XX rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma;
 XX biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;
 XX glomerulonephritis; immune deficiency syndrome; myasthenia gravis;
 XX polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;
 XX infectious disease; acquired immunodeficiency syndrome; viral infection;
 XX AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anaemia;
 XX ischaemic injury; myocardial infarction; reperfusion injury; cachexia;
 XX anorexia; stroke; cardiovascular disorder; peripheral artery disease;
 XX limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;
 XX ocular disorder; wound healing; angiogenesis; transplantation; human.
 OS Homo sapiens.
 XX WO200297033-A2.
 XX 05-DEC-2002.
 XX 07-MAY-2002; 2002WO-US014268.
 XX 25-MAY-2001; 2001US-0293473P.
 XX 04-JUN-2001; 2001US-0294981P.
 XX 02-AUG-2001; 2001US-0309176P.
 XX 21-SEP-2001; 2001US-0323807P.
 XX 09-OCT-2001; 2001US-0327364P.
 XX 07-NOV-2001; 2001US-0331044P.
 XX 14-NOV-2001; 2001US-0331310P.
 XX 20-DEC-2001; 2001US-0341237P.
 XX 03-APR-2002; 2002US-0369860P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;
 WPI; 2003-140454/13.
 XX Novel antibody useful for treating cancers and other hyperproliferative
 XX disorders, immunospecifically binds to TRAIL receptor and comprises
 XX variable heavy or light chain complementarity determining regions.
 XX Disclosure; Page 300-301; 301pp; English.
 XX The present invention relates to novel antibodies that immunospecifically
 XX bind to TRAIL receptor (TR4). Sequences of the invention are useful for
 XX treating, preventing or ameliorating cancer (e.g. colon, breast, uterine,
 XX pancreatic, lung, gastrointestinal or central nervous system cancer e.g.
 XX medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in
 XX human. They are useful for detecting expression of TR4 polypeptide and
 XX detecting, diagnosing, prognosing or monitoring cancers and other hyper-
 XX proliferative disorders. Antibodies of the invention are useful for
 XX treating, preventing or ameliorating neurodegenerative disorders (e.g.
 XX Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
 XX retinitis pigmentosa, cerebellar degeneration and Huntington's disease),
 XX immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis,
 XX Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease,
 XX polymyositis, immune-related glomerulonephritis, myasthenia gravis,
 XX Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory
 XX disorders (e.g. asthma, allergic disorders and rheumatoid arthritis),
 XX infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 XX herpes viral infections and other viral infections) and proliferative

CC disorders. They are also useful for treating myelodysplastic syndromes
 CC (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke,
 CC myocardial infarction and reperfusion injury), septic shock, cachexia,
 CC anorexia and toxin-induced liver diseases (such as alcohol). They are
 CC also useful for treating cardiovascular disorders including peripheral
 CC artery diseases such as limb ischaemia, arrhythmia, congestive heart
 CC failure and cardiovascular tuberculosis, diseases or disorders associated
 CC with neovascularisation and ocular disorders, for wound healing, for
 CC promoting angiogenesis and as adjuvants to enhance immune responsiveness
 CC to specific antigen e.g. viral antigen. They are also useful in the
 CC preparation or recovery from surgery, trauma, radiation therapy and
 CC transplantation. The present sequence is human TR4 ligand, TRAIL protein
 CC used in the invention
 XX
 XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQNI SPLVRERGQ 120
 DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQNI SPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180

QY 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKYTSYDPDPILLMKSAKNSCWSDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKYTSYDPDPILLMKSAKNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 34

ID AAO31151
 XX AAO31151 standard; protein; 281 AA.

AC AAO31151;

XX 06-OCT-2003 (first entry)

XX Human TNF-related apoptosis-inducing ligand (TRAIL).

XX Human; protein coordinate data; heavy chain variable domain; VH; cancer;
 XX complementarity determining region; CDR; light chain variable domain; VL;
 XX TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
 XX DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
 XX Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
 XX glioblastoma; graft versus host disease; antibody therapy; neutrotic;
 XX AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
 XX immunosuppressive; neuroprotective; antibody therapy; antibody.

OS Homo sapiens.

XX WO2003054216-A2.

XX 03-JUL-2003.

XX 19-DEC-2002; 2002WO-US040597.

XX 20-DEC-2001; 2001US-0341237P.

XX 05-APR-2002; 2002US-0369877P.

XX 04-JUN-2002; 2002US-0384828P.

XX 18-JUL-2002; 2002US-0396591P.

XX 15-AUG-2002; 2002US-0403370P.

PR 13-NOV-2002; 2002US-0425737P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;

XX WPI; 2003-569250/53.

XX New antibody or its fragment, useful for treating, preventing or
 XX ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
 XX gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
 XX disease, AIDS.

PS Disclosure; Page 297-298; 301pp; English.

XX The invention relates to an isolated antibody or its fragments such as
 CC VHCDR1 (heavy chain variable domain complementarity determining region),
 CC VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity
 CC determining region), VLCDR2 or VLCDR3. The antibody or its fragment
 CC immunospecifically binds TRAIL (tumour necrosis factor; TNF-related
 CC apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
 CC TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The
 CC antibody or its fragment is useful for treating, preventing or
 CC ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
 CC gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
 CC nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
 CC graft versus host disease, AIDS (acquired immune deficiency syndrome) or
 CC a neurodegenerative disorder. The invention is useful in antibody
 CC therapy. The present sequence is human TRAIL

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 1.8e-266;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQNI SPLVRERGQ 120

DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQNI SPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180

DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180

QY 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKYTSYDPDPILLMKSAKNSCWSDAEYGLY 240

DB 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKYTSYDPDPILLMKSAKNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 35

ABO25125

ID ABO25125 standard; protein; 281 AA.

XX ABO25125;

XX 05-SEP-2003 (first entry)

XX Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1.

XX Human; DNA methylation; cancer; colon cancer.

XX Homo sapiens.

XX US2003013099-A1.

XX

PD 16-JAN-2003.
 XX
 XX 07-MAR-2002; 2002US-00093766.
 XX
 XX 19-MAR-2001; 2001US-0277380P.
 XX
 XX (LASE/) LASEK A K W.
 PA (JONES/) JONES D A.
 PA (KARF/) KARPF A R.
 XX
 XX Lasek AKW, Jones DA, Karpf AR;
 PI
 XX WPI; 2003-503249/47.
 XX N-PSDB; ACD42246.
 DR
 XX
 XX New combination comprising cDNAs that are expressed in a disorder or
 PT process associated with DNA methylation, useful for diagnosing, staging,
 PT treating or monitoring treatment of cancer, e.g. colon cancer.
 PS
 XX Disclosure; Page 56-57; 66pp; English.
 XX
 XX The invention relates to a combination comprising cDNAs which are
 CC expressed in a disorder or process associated with DNA methylation. The
 CC combination and cDNAs are useful for diagnosing, staging, treating or
 CC monitoring treatment of cancer, e.g. colon cancer and for detecting
 CC changes in expression of genes encoding proteins that are associated with
 CC DNA methylation. The protein is useful for screening molecules or
 CC compounds to identify at least one ligand that binds to the protein and
 CC for producing an antibody. The present sequence represents the amino acid
 CC sequence of a protein expressed in a disorder or process associated with
 CC DNA methylation
 XX
 XX Sequence 281 AA;
 SQ
 Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESMNSPCWQVKWQLRVLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120
 DB 61 DDSYWDPNDESMNSPCWQVKWQLRVLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIREKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIREKG 180
 QY 181 FYIYISQTYFRFQBEIKENTKNDKQVYIKYKTSYDPDILLMKSARNCSWCKDAEYGLY 240
 DB 181 FYIYISQTYFRFQBEIKENTKNDKQVYIKYKTSYDPDILLMKSARNCSWCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 36
 ID ADB61471
 XX ADB61471 standard; protein; 281 AA.
 AC ADB61471;
 XX
 XX 04-DEC-2003 (first entry)
 XX
 XX Native human Apo-2 ligand protein.
 XX
 XX Apo-2 ligand; DR5, Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW

KW native; human.
 XX Homo sapiens.
 OS
 XX WO2003029420-A2.
 PN
 XX 10-APR-2003.
 XX
 XX 01-OCT-2002; 2002WO-US031210.
 XX
 XX 02-OCT-2001; 2001US-0326622P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Kelley RF, Lindstrom SH;
 PI
 XX WPI; 2003-541400/51.
 XX N-PSDB; ADB61470.
 DR
 XX
 XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
 PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.
 PS
 XX Claim 1; Fig 1; 92pp; English.
 XX
 XX The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5, Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, D116C, N134C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5, Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5, Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the native human Apo-2 ligand protein of
 CC the invention.
 XX
 XX Sequence 281 AA;
 SQ
 Query Match 100.0%; Score 281; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESMNSPCWQVKWQLRVLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120
 DB 61 DDSYWDPNDESMNSPCWQVKWQLRVLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIREKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIREKG 180
 QY 181 FYIYISQTYFRFQBEIKENTKNDKQVYIKYKTSYDPDILLMKSARNCSWCKDAEYGLY 240
 DB 181 FYIYISQTYFRFQBEIKENTKNDKQVYIKYKTSYDPDILLMKSARNCSWCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 RESULT 37
 ADC35202
 ID ADC35202 standard; protein; 281 AA.
 AC ADC35202;
 XX
 DT 18-DEC-2003 (first entry)
 DE Human TNF ligand family member #10.
 KW human; tumour necrosis factor; TNF ligand; endokine alpha;
 KW excessive bone resorption disorder; osteoporosis; Paget's disease;
 KW arterial calcification.
 XX
 OS Homo sapiens.
 PN US2003100074-A1.
 PD 29-MAY-2003.
 XX
 PF 15-AUG-2002; 2002US-00218547.
 PR 16-AUG-2001; 2001US-0312542P.
 PR 30-OCT-2001; 2001US-0330761P.
 XX
 PA (YUGG/) YU G.
 PA (NIJJ/) NI J.
 PA (ROSE/) ROSEN C A.
 PA (NARD/) NARDELLI B.
 XX
 PI Yu G, Ni J, Rosen CA, Nardelli B;
 XX
 DR WPI; 2003-696072/66.
 DR N-PSDB; ADC35201.
 XX
 PT New Endokine alpha gene useful for preparing a composition for treating a
 PT disease associated with excessive or insufficient bone resorption e.g.,
 PT osteoporosis, Paget's disease or arterial calcification.
 XX
 PS Disclosure; SEQ ID NO 20; 145pp; English.
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC tumour necrosis factor family ligand. A composition comprising the
 CC isolated antibody or its fragment is used for treating an individual in
 CC need of decreased level of endokine alpha activity. The endokine alpha
 CC polypeptide present in a heterotrimeric complex is used for treating an
 CC individual having a disorder associated with excessive bone resorption,
 CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an
 CC individual having a disorder associated with insufficient bone resorption
 CC comprises administering an endokine alpha antagonist, which is the
 CC antibody that binds specifically to endokine alpha polypeptide. The
 CC present sequence represents the amino acid sequence of a tumour necrosis
 CC factor family ligand.
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTYVTNELKQMDKYSGGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTYVTNELKQMDKYSGGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVKQLRQVLMILRTSEETISTVQEKQONISPLVREGPQ 120

DB 61 DDSYWDPNDEESMNSPCWQVKQLRQVLMILRTSEETISTVQEKQONISPLVREGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 RESULT 38
 ADD14080
 ID ADD14080 standard; protein; 281 AA.
 XX
 AC ADD14080;
 XX
 DT 01-JAN-2004 (first entry)
 DE Human src biomarker polypeptide SEQ ID NO:269.
 KW predictor set; protein tyrosine kinase activity modulator;
 KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
 KW gene therapy; drug sensitivity; genetic profile; cancer; human.
 XX
 OS Homo sapiens.
 XX WO2003062395-A2.
 PN 31-JUL-2003.
 PD
 XX
 PF 17-JAN-2003; 2003WO-US001981.
 PR 18-JAN-2002; 2002US-0350061P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Huang F, Fairchild CR, Lee FY, Shaw P;
 XX WPI; 2003-636735/60.
 DR N-PSDB; ADD14676.
 XX
 PT New polynucleotides and polypeptides for predicting the activity of
 PT compounds that interact with protein tyrosine kinases and/or protein
 PT tyrosine kinase pathways.
 XX
 PS Claim 10; SEQ ID NO 269; 139pp; English.
 CC The present invention describes a predictor set comprising a plurality of
 CC polynucleotides or polypeptides whose expression pattern is predictive of
 CC the response of cells to treatment with a compound that modulates protein
 CC tyrosine kinase activity or members of the protein tyrosine kinase
 CC pathway. Also described: (1) predicting whether a compound is capable of
 CC modulating the activity of cells, comprising obtaining a sample of cells,
 CC determining whether the cells express a plurality of markers, and
 CC correlating the expression of the markers to the compound's ability to
 CC modulate the activity of the cells; (2) a plurality of cell lines for
 CC identifying polynucleotides and polypeptides whose expression levels
 CC correlate with compound sensitivity or resistance of cells associated
 CC with a disease state; and (3) identifying polynucleotides and
 CC polypeptides that predict compound sensitivity or resistance of cells
 CC associated with a disease state, comprising subjecting the plurality of
 CC cell lines to one or more compounds, analysing the expression pattern of
 CC a microarray of polynucleotides or polypeptides, and selecting
 CC polynucleotides or polypeptides that predict the sensitivity or
 CC resistance of cells associated with a disease state by using the
 CC expression pattern of the microarray. The polynucleotides and
 CC polypeptides have cytostatic activities, and can be used in gene therapy.
 CC The polynucleotides and polypeptides are useful in predicting the

CC activity of compounds that interact with protein tyrosine kinases and/or
 CC protein tyrosine kinase pathways. These may be used in determining drug
 CC sensitivity in patients to allow the development of individualized
 CC genetic profiles which aid in treating diseases and disorders (e.g.
 CC cancer) based on patient response at a molecular level. The present
 CC sequence is used in the exemplification of the present invention.

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTSPLVREGPQ 120
 DB 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTSPLVREGPQ 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 180
 QY 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLY 240
 DB 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 39

ID ADD19010
 AC ADD19010 standard; protein; 281 AA.

XX ADD19010;

DT 15-JAN-2004 (first entry)

XX Human disease related protein SeqID499.

XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
 KW antiarteriosclerotic; vulnary; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transportation; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing.

XX Homo sapiens.

XX W02003018621-A2.

XX 06-MAR-2003.

XX 23-AUG-2002; 2002W0-GB003892.

XX 23-AUG-2001; 2001GB-00020558.

XX 05-OCT-2001; 2001GB-00024037.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX WPI; 2003-290046/28.

XX N-PSDB; ADD19011.

XX New substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion

PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.

XX Claim 25; SEQ ID NO 499; 424pp; English.

XX This invention relates to novel human genes and gene product which are
 CC implicated in certain disease states. Compounds which modulate the
 CC proteins of the invention may have cytostatic, antiinflammatory, the
 CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
 CC sequences of the invention may be useful for gene therapy. The invention
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
 CC erythropoiesis, or the biological response to hypoxia conditions
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transportation, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein of the invention.

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTSPLVREGPQ 120
 DB 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTSPLVREGPQ 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 180
 QY 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLY 240
 DB 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 40

ADE76953

ID ADE76953 standard; protein; 281 AA.

XX ADE76953;

XX 29-JAN-2004 (first entry)

XX Human protein expressed in a liver disorder #32.

XX human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
 KW tumour; liver; inflammatory disorder; immune response disorder;
 KW high-throughput screening; differential gene expression; gene therapy.

XX Homo sapiens.

XX US2003108871-A1.

XX 12-JUN-2003.

XX 30-JUL-2001; 2001US-00919039.

XX 28-JUL-2000; 2000US-0222113P.

XX (KASE/) KASER M R.

PI Kaser MR;
 DR WPI; 2004-031227/03.
 DR N-PSDB; ADE76952.
 XX
 XX Composition comprising several cDNAs that are differentially expressed in
 PT treated human C3A liver cell cultures, useful for treating liver
 PT disorders.
 XX
 XX Claim 1; SEQ ID NO 118; 41pp; English.
 XX
 XX The invention relates to a composition comprising several cDNAs that are
 CC differentially expressed in a liver disorder. The composition is useful
 CC for treating liver disorder such as hyperlipidaemia, hypertension, type
 CC II diabetes, tumours of the liver and disorders of the inflammatory and
 CC immune response. The composition is useful for a high-throughput method
 CC of screening several molecules or compounds to identify a ligand which
 CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
 CC high-throughput method for using a protein to screen several molecules or
 CC compounds to identify at least one ligand which specifically binds the
 CC protein which involves combining the protein encoded by the cDNA with
 CC several of molecules or compounds under conditions to allow specific
 CC binding, and detecting specific binding between the protein and a
 CC molecule or compound, therefore identifying a ligand which specifically
 CC binds the protein. The composition is useful for detecting and
 CC quantifying differential gene expression, can be used in gene therapy, to
 CC formulate prognosis and to design a treatment regimen and to monitor the
 CC efficacy of treatment. The present sequence represents the amino acid
 CC sequence of a protein encoded by a cDNA differentially expressed in a
 CC liver disorder.
 XX
 XX Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1. MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKE 60
 Db 1. MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKE 60
 QY 61. DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVREGPQ 120
 Db 61. DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVREGPQ 120
 QY 121. RVAHITGRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180
 Db 121. RVAHITGRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180
 QY 181. FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKARSNCWSKDAEYGLY 240
 Db 181. FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKARSNCWSKDAEYGLY 240
 QY 241. SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241. SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 41
 AAW76332
 ID AAW76332 standard; protein; 279 AA.
 XX
 AC AAW76332;
 XX
 XX 11-JAN-1999 (first entry)
 DE Human TL2 (TRAIL), ligand for TR5.
 KW TL2; TRAIL; tumour necrosis related receptor; TR5; inflammation;
 KW arthritis; septicaemia; transplant rejection; autoimmune disease;
 KW inflammatory bowel disease; graft versus host disease; infection; stroke;
 KW ischaemia; acute respiratory disease syndrome; psoriasis; restenosis;
 KW brain injury; AIDS; bone disease; cancer; atherosclerosis;

KW Alzheimer's disease; human; therapy; diagnosis; ligand.
 XX Homo sapiens.
 XX EP867509-A2.
 XX 30-SEP-1998.
 XX 04-FEB-1998; 98EP-00300827.
 XX 05-FEB-1997; 97US-00795910.
 XX 28-JUL-1997; 97US-00901469.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Young PR, Tan KB, Truneh A, Lyn SDP;
 XX WPI; 1998-497862/43.
 XX New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent
 PT and treat e.g. inflammation, arthritis, septicaemia, autoimmune diseases,
 PT infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury,
 PT AIDS and bone diseases.
 XX Disclosure; Page 17-18; 22pp; English.
 XX This is the amino acid sequence of human TL2 (also known as TRAIL), which
 CC has newly been discovered to be a ligand of human tumour necrosis related
 CC receptor TR5 (see AAW76331). This TR5 polypeptide of the invention and
 CC TL2 can be used in screening processes for compounds which bind the
 CC receptor, or its ligand, and which activate (agonists) or inhibit
 CC (antagonists) the receptor or TR5. Treatment of a subject with the need
 CC to inhibit TR5 polypeptide activity comprises administering an antagonist
 CC to the polypeptide, administering a nucleic acid that inhibits the
 CC expression of the nucleotide sequence encoding the polypeptide and/or
 CC administering a polypeptide that competes with the polypeptide for its
 CC ligand, substrate or receptor. The active agents can be used for the
 CC treatment of chronic and acute inflammation, arthritis, septicaemia,
 CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),
 CC transplant rejection, graft vs host disease, infection, stroke,
 CC ischaemia, acute respiratory disease syndrome, restenosis, brain injury,
 CC AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders),
 CC atherosclerosis and Alzheimer's disease
 XX
 XX Sequence 279 AA;
 Query Match 99.3%; Score 279; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.6e-264;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3. MMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKEDD 62
 Db 1. MMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKEDD 60
 QY 63. SYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVREGPQV 122
 Db 61. SYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVREGPQV 120
 QY 123. AAHITGRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVHEKGFY 182
 Db 121. AAHITGRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVHEKGFY 180
 QY 183. YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKARSNCWSKDAEYGLY 242
 Db 181. YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKARSNCWSKDAEYGLY 240
 QY 243. YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241. YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279
 RESULT 42
 AAW95032

AAW95032 standard; protein; 279 AA.
AAW95032;
13-MAY-1999 (first entry)
Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.
Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;
inflammation; septicemia; autoimmune disease; transplant rejection;
graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
acute respiratory disease syndrome; restenosis, bone disease; cancer;
atherosclerosis; Alzheimer's disease.
Unidentified.
EP897114-A2.
17-FEB-1999.
04-JUN-1998; 98EP-00304424.
13-AUG-1997; 97US-0055513P.
26-AUG-1997; 97US-0056980P.
29-AUG-1997; 97US-0057550P.
(SMIK) SMITHKLINE BEECHAM CORP.
Brigham-Burke MR, Young PR;
WPI; 1999-134308/12.
Identifying agonists and antagonists to tumour necrosis factor receptor
(TNF-R) related polypeptides (LRI, LR2, LT2 and LT4) - useful for
treating stroke, Alzheimer's disease and AIDS.
Disclosure; Page 14-15; 18pp; English.
The invention relates to identifying agonists or antagonists to tumour
necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2
or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)
assessing the ability of the candidate compound to compete with TR1 or
TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful
for treating diseases caused by imbalance of TR or TR polypeptide levels,
which cause: chronic and acute inflammation, arthritis, septicemia,
autoimmune diseases, transplant rejection, graft vs. host disease,
infection, stroke, ischemia, acute respiratory disease syndrome,
restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and
Alzheimer's disease. The present sequence represents a TNF-R related
polypeptide TL2
Sequence 279 AA;
Query Match 99.3%; Score 279; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e-264;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MMEVQGGPSLGQTCVLIVFTVLQSLCAVTVYVFTNELKQMDKYSGIACFLKEDD 62
DB 1 MMEVQGGPSLGQTCVLIVFTVLQSLCAVTVYVFTNELKQMDKYSGIACFLKEDD 60
QY 63 SYNDPNDDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRGFRQV 122
DB 61 SYNDPNDDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRGFRQV 120
QY 123 AAHTGTGRSNTLSSPNKXKALGRKINSWSSRSGHSFLNLHRLNGELVIHEKGFY 182
DB 121 AAHTGTGRSNTLSSPNKXKALGRKINSWSSRSGHSFLNLHRLNGELVIHEKGFY 180
QY 183 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSGARNCSWSKDAEYGLYSI 242
AAW95032 standard; protein; 279 AA.
AAW95032;
13-MAY-1999 (first entry)
Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.
Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;
inflammation; septicemia; autoimmune disease; transplant rejection;
graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
acute respiratory disease syndrome; restenosis, bone disease; cancer;
atherosclerosis; Alzheimer's disease.
Unidentified.
EP897114-A2.
17-FEB-1999.
04-JUN-1998; 98EP-00304424.
13-AUG-1997; 97US-0055513P.
26-AUG-1997; 97US-0056980P.
29-AUG-1997; 97US-0057550P.
(SMIK) SMITHKLINE BEECHAM CORP.
Brigham-Burke MR, Young PR;
WPI; 1999-134308/12.
Identifying agonists and antagonists to tumour necrosis factor receptor
(TNF-R) related polypeptides (LRI, LR2, LT2 and LT4) - useful for
treating stroke, Alzheimer's disease and AIDS.
Disclosure; Page 14-15; 18pp; English.
The invention relates to identifying agonists or antagonists to tumour
necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2
or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)
assessing the ability of the candidate compound to compete with TR1 or
TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful
for treating diseases caused by imbalance of TR or TR polypeptide levels,
which cause: chronic and acute inflammation, arthritis, septicemia,
autoimmune diseases, transplant rejection, graft vs. host disease,
infection, stroke, ischemia, acute respiratory disease syndrome,
restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and
Alzheimer's disease. The present sequence represents a TNF-R related
polypeptide TL2
Sequence 279 AA;
Query Match 99.3%; Score 279; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e-264;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MMEVQGGPSLGQTCVLIVFTVLQSLCAVTVYVFTNELKQMDKYSGIACFLKEDD 62
DB 1 MMEVQGGPSLGQTCVLIVFTVLQSLCAVTVYVFTNELKQMDKYSGIACFLKEDD 60
QY 63 SYNDPNDDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRGFRQV 122
DB 61 SYNDPNDDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRGFRQV 120
QY 123 AAHTGTGRSNTLSSPNKXKALGRKINSWSSRSGHSFLNLHRLNGELVIHEKGFY 182
DB 121 AAHTGTGRSNTLSSPNKXKALGRKINSWSSRSGHSFLNLHRLNGELVIHEKGFY 180
QY 183 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSGARNCSWSKDAEYGLYSI 242

Db 181 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSGARNCSWSKDAEYGLYSI 240
QY 243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 281
Db 241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 279
RESULT 43
AAW27018
ID AAW27018 standard; protein; 281 AA.
XX AC AAW27018;
XX DT 24-SEP-1999 (first entry)
XX DE Human Apo-2 ligand (Apo-2L) variant D269A.
XX KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
XX KW lupus; immune-mediated glomerular nephritis; human; variant.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 269 /label= D269A
FT FT /note= "wild-type Asp is replaced with Ala"
XX PN WO9936535-A1.
XX PD 22-JUL-1999.
XX PF 15-JAN-1999; 99WO-US001039.
XX PR 15-JAN-1998; 98US-00007886.
XX PR 15-APR-1998; 98US-00060533.
XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;
XX WPI; 1999-444397/37.
XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
in mammalian cancer cells.
XX Claim 11; Page; 86pp; English.
XX The invention relates to a novel human cytokine, designated Apo-2 ligand
(Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
cells. This is useful for the treatment of cancer. Apo-2L can be used to
induce apoptosis for pathological conditions characterized by decreased
levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
coding sequence can also be used in quantitative and screening diagnostic
techniques. Anti-Apo-2L antibodies can be used for treating diseases
associated with increased apoptosis. Sequences AAY27016-19 represent
specific examples of Apo-2L variants. Note: This sequence is not provided
in the specification. It has been created by modifying the wild-type Apo-
2L sequence provided in Fig 1A
XX Sequence 281 AA;
Query Match 95.4%; Score 268; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 9.6e-254;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYDPNDDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRGFRQV 120

Db 61 DSYWDPNDEESNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNISPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRGHGFSLNHLRNGELVIHEKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRGHGFSLNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRQEEIKENTKNDKQWQVIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRQEEIKENTKNDKQWQVIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDM 268
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDM 268

RESULT 44

ADB61495
 ID ADB61495 standard; protein; 281 AA.

XX AC ADB61495;
 XX DT 04-DEC-2003 (first entry)
 XX DE Human Apo-2 ligand protein mutant H264C.
 XX KW Apo-2 ligand; DR5-Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX OS Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 264 /note= "Native residue of His is substituted by Cys"
 FT WO2003029420-A2.
 XX 10-APR-2003.
 PF 01-OCT-2002; 2002WO-US031210.
 XX 02-OCT-2001; 2001US-0326622P.
 XX (GETH) GENENTECH INC.
 XX Kelley RF, Lindstrom SH;
 DR WPI; 2003-541400/51.
 XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
 PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.
 XX Claim 1; Page; 92pp; English.

CC The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5-Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, E140C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5-Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5-Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,

CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant H264C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.

XX Sequence 281 AA;

Query Match 93.6%; Score 263; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 7.5e-249;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGGTGVILVIFVTLVLOSCLVAVTVVYFTNELKQWQDKYSKGIACFLKE 60
 Db 1 MAMMEVQGGPSLGGTGVILVIFVTLVLOSCLVAVTVVYFTNELKQWQDKYSKGIACFLKE 60
 QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNISPLVRERGQ 120
 Db 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNISPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRGHGFSLNHLRNGELVIHEKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRGHGFSLNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRQEEIKENTKNDKQWQVIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRQEEIKENTKNDKQWQVIYKYTSYPPDPILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNE 263
 Db 241 SIYQGGIFELKENDRIFVSVTNE 263

RESULT 45

ADB61494
 ID ADB61494 standard; protein; 281 AA.
 XX AC ADB61494;
 XX DT 04-DEC-2003 (first entry)
 XX DE Human Apo-2 ligand protein mutant E263C.

XX KW Apo-2 ligand; DR5-Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX OS Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 263 /note= "Native residue of Glu is substituted by Cys"
 FT WO2003029420-A2.
 XX 10-APR-2003.
 XX 01-OCT-2002; 2002WO-US031210.
 XX 02-OCT-2001; 2001US-0326622P.

XX PA (GETH) GENENTECH INC.
 XX PI Kelley RF, Lindstrom SH;
 XX DR WPI; 2003-541400/51.
 XX
 PT Novel isolated Apo-2 ligand variant polypeptide useful for treating
 PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.
 XX
 PS Claim 1; Page; 92pp; English.
 XX
 CC The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, S153C, R170C,
 CC R170K, R170S, K179C, E249C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant E263C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.

XX Sequence 281 AA;

Query Match 93.2%; Score 262; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 7.2e-248;
 Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 Db 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMLTSETISTVQEKQNTSPLVREGPQ 120
 Db 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMLTSETISTVQEKQNTSPLVREGPQ 120
 QY 121 RVAAHITGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
 Db 121 RVAAHITGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
 QY 181 FYYISQTYFRFOBEIKENTKNDKQVQYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 Db 181 FYYISQTYFRFOBEIKENTKNDKQVQYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTN 262
 Db 241 SIYGGIFELKENDRIFVSVTN 262

RESULT 46
 ADB61493
 ID ADB61493 standard; protein; 281 AA.

XX AC ADB61493;
 XX DT 04-DEC-2003 (first entry)
 XX DE Human Apo-2 ligand protein mutant R255C.
 XX
 KW Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 255 /note= "Native residue of Arg is substituted by Cys"
 FT
 XX WO2003029420-A2.
 PD 10-APR-2003.
 XX
 XX 01-OCT-2002; 2002WO-US031210.
 XX
 XX 02-OCT-2001; 2001US-0326622P.
 XX (GETH) GENENTECH INC.
 PA Kelley RF, Lindstrom SH;
 PI WPI; 2003-541400/51.
 DR
 XX
 PT Novel isolated Apo-2 ligand variant polypeptide useful for treating
 PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.
 XX
 PS Claim 1; Page; 92pp; English.
 CC
 CC The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, S153C, R170C,
 CC R170K, R170S, K179C, E249C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant R255C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.
 XX
 SQ Sequence 281 AA;

Query Match 90.4%; Score 254; DB 7; Length 281;

Best Local Similarity 100.0%; Pred. No. 4.8e-240;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYDNDPDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPQ 120
DB 61 DDSYDNDPDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYPPDILLMKSGARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYPPDILLMKSGARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKEND 254
DB 241 SIYQGGIFELKEND 254

RESULT 47

ADB61492
ID ADB61492 standard; protein; 281 AA.
AC ADB61492;
DT 04-DEC-2003 (first entry)
DE Human Apo-2 ligand protein mutant E249C.
KW Apo-2 ligand; DR5 Apo2L complex; receptor contact region;
KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW human; mutant; mutein.
OS Synthetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 249 /note= "Native residue of Glu is substituted by Cys"
XX
XX
PN WO2003029420-A2.
XX
PD 10-APR-2003.
XX
PF 01-OCT-2002; 2002WO-US031210.
XX
PR 02-OCT-2001; 2001US-0326622P.
XX
PA (GETH) GENENTECH INC.
XX
PI Kelley RF, Lindstrom SH;
XX
DR WPI; 2003-541400/51.
XX
PT Novel isolated Apo-2 ligand variant polypeptide useful for treating
PT cancer or an immune-related disease such as multiple sclerosis, comprises
PT amino acid substitutions in the native sequence of the Apo-2 ligand.
XX
PS Claim 1; Page; 92pp; English.
XX
CC The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide having a sequence that differs from the native sequence
CC having 281 amino acids given in specification. The Apo-2 ligand variant
CC polypeptide is selected from a polypeptide having substitutions at
CC residue positions identified from x-ray crystal structure of the
CC DR5 Apo2L complex. The polypeptide having the substitutions made at

CC residue position(s) selected from 20 positions such as S96C, S101C,
CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
CC residue position is, outside of the receptor contact region of the
CC DR5 Apo2L complex, and displays high solvent accessibility in the crystal
CC structure of the DR5 Apo2L complex. The Apo-2 ligand variant polypeptide
CC and further compositions have the following activities: cytosolic,
CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
CC inducing apoptosis in mammalian cells, by exposing mammalian cells
CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
CC immune-related disease (such as arthritis or multiple sclerosis) in a
CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the human Apo-2 ligand mutant E249C
CC protein of the invention. NOTE: This sequence is not shown in the
CC specification. It has been created from information provided in Claim 1
CC and from the sequence in Fig 1 of the specification.

XX Sequence 281 AA;

Query Match 88.3%; Score 248; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.6e-234;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYDNDPDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPQ 120
DB 61 DDSYDNDPDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYPPDILLMKSGARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYPPDILLMKSGARNSCWSDAEYGLY 240

QY 241 SIYQGGIF 248
DB 241 SIYQGGIF 248

RESULT 48

AAV01516
ID AAV01516 standard; peptide; 281 AA.
XX
XX AAV01516;
DT 27-MAY-1999 (first entry)
XX
XX Protein associated with neurodegenerative and autoimmune diseases.
DR
KW Neurodegenerative disease; autoimmune disease; inflammatory disease;
KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
KW surface receptor; TRAIL protein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 245 /note= "Gly or Cys"
XX
PN FR2766713-A1.
XX

PD 05-FEB-1999.
 XX
 PF 04-AUG-1997; 97FR-000101176.
 XX
 PR 04-AUG-1997; 97FR-000101176.
 XX
 PA (INMR) BIO MERIEUX.
 XX
 PI Rieger F, Belliveau JF, Perron H;
 XX
 XX WPI; 1999-156177/14.
 XX
 DR Use of polypeptide derived from TRAIL protein for diagnosis of
 PT degenerative disease - autoimmunity and inflammation, also useful in
 PT prevention or treatment, and similar use of corresponding ligand and
 PT nucleic acid.
 XX
 XX Claim 1; Page 13; 21pp; French.
 XX
 XX The specification describes the use a polypeptide corresponding to at
 CC least the primary sequence of part of the present sequence to produce a
 CC diagnostic, prophylactic or therapeutic composition useful in cases of
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
 CC be used in treatment of neurodegenerative disease, lupus erythematosus,
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
 CC nervous system cells, antigenic and specifically recognise the surface
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
 CC receptors, inhibiting formation of natural complex
 XX
 XX Sequence 281 AA;
 SQ
 Query Match 86.8%; Score 244; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3e-230;
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACPLKE 60
 Db 1 MAMMEVGGPSLGTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACPLKE 60
 QY 61 DDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIISPLVRERGQ 120
 Db 61 DDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIISPLVRERGQ 120
 QY 121 RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
 Db 121 RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPPILLMKSRNSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPPILLMKSRNSCWSKDAEYGLY 240
 QY 241 SIYQ 244
 Db 241 SIYQ 244
 RESULT 49
 AA72935
 ID AA72935 standard; protein; 266 AA.
 XX
 AC AA72935;
 XX
 DT 11-SEP-2003 (revised)
 DT 13-JUN-2001 (first entry)
 XX
 DE OmpA signal peptide-human TRAIL fusion protein.
 XX
 XX Human; attenuated tumour-targeted bacteria; effector molecule;
 KW tumour necrosis factor; TNF; anti-angiogenic factor;
 KW cytotoxic polypeptide; tumour inhibitory enzyme; therapy; carcinoma;
 KW melanoma; lymphoma; sarcoma; metastasis; cytostatic; fusion protein;

TNF-alpha-related apoptosis-inducing ligand; TRAIL.
 KW
 XX Homo sapiens.
 OS Escherichia coli.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= OmpA_signal_peptide
 FT 23..266
 FT /note= "Mature human TNF-alpha-related apoptosis-inducing
 FT ligand"
 XX
 XX W0200125397-A2.
 PN
 XX
 XX 12-APR-2001.
 PD
 XX
 XX 24-AUG-2000; 2000WO-US023242.
 XX
 XX 04-OCT-1999; 99US-0157500P.
 PR 04-OCT-1999; 99US-0157581P.
 PR 04-OCT-1999; 99US-0157637P.
 XX
 XX (VION-) VION PHARM INC.
 PA
 XX Bermudes DG, King IC, Clairmont CA, Lin SL, Belcourt M;
 PI
 XX WPI; 2001-245063/25.
 XX N-PSDB; AAD03112.
 DR
 XX Attenuated tumor-targeted bacteria comprising nucleic acids encoding
 PT primary and secondary effector molecules, useful for the treatment of
 PT e.g. carcinomas, melanomas, lymphomas and sarcomas.
 XX
 XX Example 7; Fig 6; 185pp; English.
 PS
 XX The present invention relates to the preparation and use of attenuated
 CC tumour-targeted bacteria, such as, e.g., Salmonella, as a vector for the
 CC delivery of one or more primary effector molecules and secondary effector
 CC molecules to the site of a solid tumour. The primary effector molecules
 CC of the invention include members of the tumour necrosis factor (TNF),
 CC anti-angiogenic factors, cytotoxic polypeptides and tumour inhibitory
 CC enzymes. They induce a local immune response at the site of the tumour
 CC that results in the inhibition of growth of a tumour or tumour cells. The
 CC primary effector molecules are used for the treatment of solid tumours
 CC such as carcinomas, melanomas, lymphomas, sarcomas or metastases derived
 CC from these tumours. The present sequence is OmpA signal peptide-mature
 CC human TNF-alpha-related apoptosis-inducing ligand (TRAIL) fusion protein.
 CC The fusion of OmpA signal peptide to the amino terminus of TRAIL effector
 CC molecule enhances the periplasmic localisation and subsequent processing
 CC of the effector molecule. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 266 AA;

Query Match 86.1%; Score 242; DB 4; Length 266;
 Best Local Similarity 100.0%; Pred. No. 2.6e-228;
 Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 40 NELKQMDKYSGIACFLKEDDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSEET 99
 Db 25 NELKQMDKYSGIACFLKEDDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSEET 84
 QY 100 ISTVQEKQNIISPLVRERGQVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRS 159
 Db 85 ISTVQEKQNIISPLVRERGQVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRS 144
 QY 160 GHSFSLNHLRNGELVTHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPP 219
 Db 145 GHSFSLNHLRNGELVTHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPP 204
 QY 220 ILLMKSRNSCWSKDAEYGLIYQGGIFELKENDRIFVSVTNEHLIDMDHASFPGAPL 279

Db 205 ILLMKARNCSWDAEYGLISYIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGFL 264

QY 280 VG 281
||
Db 265 VG 266

RESULT 50
ADB61491
ID ADB61491 standard; protein; 281 AA.
XX ADB61491;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human Apo-2 ligand protein mutant D234C.
XX
KW Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW human; mutant; muten.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 234
FT /note= "Native residue of Asp is substituted by Cys"
XX
XX WO2003029420-A2.
XX
XX 10-APR-2003.
XX
XX 01-OCT-2002; 2002WO-US031210.
XX
XX 02-OCT-2001; 2001US-0326622P.
XX
XX (GETH) GENENTECH INC.
XX
XX Kelley RF, Lindstrom SH;
XX
XX WPI; 2003-541400/51.
XX
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
XX cancer or an immune-related disease such as multiple sclerosis, comprises
XX amino acid substitutions in the native sequence of the Apo-2 ligand.
XX
XX Claim 1; Page; 92pp; English.
XX
XX The invention relates to a novel isolated Apo-2 ligand variant
XX polypeptide having a sequence that differs from the native sequence
XX having 281 amino acids given in specification. The Apo-2 ligand variant
XX polypeptide is selected from a polypeptide having substitutions at
XX residue positions identified from x-ray crystal structure of the
XX DR5.Apo2L complex. The polypeptide having the substitutions made at
XX residue position(s) selected from 20 positions such as S96C, S101C,
XX S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
XX R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
XX residue position is, outside of the receptor contact region of the
XX DR5.Apo2L complex, and displays high solvent accessibility in the crystal
XX structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
XX and further compositions have the following activities: cytostatic,
XX antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
XX an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
XX inducing apoptosis in mammalian cells, by exposing mammalian cells
XX expressing a receptor selected from DR4 receptor and DR5 receptor to a
XX therapeutically effective amount of the Apo-2 ligand variant polypeptide,
XX Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
XX colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
XX the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
XX treating cancer (such as lung, breast, colon or colorectal cancer) or an
XX immune-related disease (such as arthritis or multiple sclerosis) in a

CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the human Apo-2 ligand mutant D234C
CC protein of the invention. NOTE: This sequence is not shown in the
CC specification. It has been created from information provided in claim 1
CC and from the sequence in Fig 1 of the specification.
XX
SQ Sequence 281 AA;
Query Match 82.9%; Score 233; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.7e-219;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGSPSLGQTCVLIVIFVTLQSLCAVAVYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVGGSPSLGQTCVLIVIFVTLQSLCAVAVYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCQVQKWLQRLVRKWLMTSETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDNDDESMNSPCQVQKWLQRLVRKWLMTSETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDPPILLMKSAARNCSWSK 233
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDPPILLMKSAARNCSWSK 233

RESULT 51
RAY27017
ID AAY27017 standard; protein; 281 AA.
XX
XX AC AAY27017;
XX
XX 24-SEP-1999 (first entry)
XX
XX Human Apo-2 ligand (Apo-2L) variant D218A.
XX
XX Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
XX lupus; immune-mediated glomerular nephritis; human; variant.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 218
XX /label= D218A
XX /note= "wild-type Asp is replaced with Ala"
XX
XX WO9936535-A1.
XX
XX 22-JUL-1999.
XX
XX 15-JAN-1999; 99WO-US001039.
XX
XX 15-JAN-1998; 98US-00007886.
XX
XX 15-APR-1998; 98US-00060533.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;
XX WPI; 1999-444397/37.
XX
XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
XX in mammalian cancer cells.
XX
XX Claim 10; Page; 86pp; English.
XX
XX The invention relates to a novel human cytokine, designated Apo-2 ligand
XX (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant

methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-2L can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like lupus and immune-mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic techniques. Anti-Apo-2L antibodies can be used for treating diseases associated with increased apoptosis. Sequences AAY27016-19 represent specific examples of Apo-2L variants. Note: This sequence is not provided in the specification. It has been created by modifying the wild-type Apo-2L sequence provided in Fig 1A

XX Sequence 281 AA;

Query Match 77.2%; Score 217; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 8e-204;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLQGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVGGPSLQGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DDSYWDNDDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
QY 181 FYYISQTYFRFOEIKENTKNDKQWQYIYKYTSYP 217
DB 181 FYYISQTYFRFOEIKENTKNDKQWQYIYKYTSYP 217

RESULT 52

AAY27019

ID AAY27019 standard; protein; 281 AA.

XX AAY27019;

XX 24-SEP-1999 (first entry)

XX Human Apo-2 ligand (Apo-2L) variant D203A, D218A, D269A.

XX Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;

XX lupus; immune-mediated glomerular nephritis; human; variant.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 203 /label= D203A

FT /note= "wild-type Asp is replaced with Ala"

FT Misc-difference 218

FT /label= D218A

FT /note= "wild-type Asp is replaced with Ala"

FT Misc-difference 269

FT /label= D269A

FT /note= "wild-type Asp is replaced with Ala"

XX WO9936535-A1.

XX 22-JUL-1999.

XX 15-JAN-1999; 99WO-US001039.

XX 15-JAN-1998; 98US-00007886.

XX 15-APR-1998; 98US-00060533.

XX (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;

XX WPI; 1999-444397/37.

XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis

XX in mammalian cancer cells.

XX Claim 12; Page; 86pp; English.

XX The invention relates to a novel human cytokine, designated Apo-2 ligand (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-2L can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like lupus and immune-mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic techniques. Anti-Apo-2L antibodies can be used for treating diseases associated with increased apoptosis. Sequences AAY27016-19 represent specific examples of Apo-2L variants. Note: This sequence is not provided in the specification. It has been created by modifying the wild-type Apo-2L sequence provided in Fig 1A

XX Sequence 281 AA;

Query Match 71.9%; Score 202; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-189;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLQGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVGGPSLQGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDNDDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120

DB 61 DDSYWDNDDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180

DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180

QY 181 FYYISQTYFRFOEIKENTKN 202

DB 181 FYYISQTYFRFOEIKENTKN 202

RESULT 53

AAY27016

ID AAY27016 standard; protein; 281 AA.

XX AAY27016;

XX 24-SEP-1999 (first entry)

XX Human Apo-2 ligand (Apo-2L) variant D203A.

XX Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;

XX lupus; immune-mediated glomerular nephritis; human; variant.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 203

FT /label= D203A

FT /note= "wild-type Asp is replaced with Ala"

XX WO9936535-A1.

XX 22-JUL-1999.

XX 15-JAN-1999; 99WO-US001039.

XX

PR 15-JAN-1998; 98US-00007886.
 PR 15-APR-1998; 98US-00060533.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;
 XX WPI; 1999-444397/37.
 DR A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 XX in mammalian cancer cells.
 PT Claim 9; Page; 86pp; English.
 PS The invention relates to a novel human cytokine, designated Apo-2 ligand
 XX (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis. Sequences AAY27016-19 represent
 CC specific examples of Apo-2L variants. Note: This sequence is not provided
 CC in the specification. It has been created by modifying the wild-type Apo-
 CC 2L sequence provided in Fig 1A
 XX Sequence 281 AA;
 SQ

Query Match 71.9%; Score 202; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-189;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DSDYDNDPNDDESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
 DB 61 DSDYDNDPNDDESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 QY 181 FYIYISQTYFRFQBEIKENTKN 202
 DB 181 FYIYISQTYFRFQBEIKENTKN 202

RESULT 54
 ABG72257
 ID ABG72257 standard; protein; 281 AA.
 XX AC ABG72257;
 XX DT 04-MAR-2003 (first entry)
 XX Human tumour related apoptosis inducing ligand (Trail).
 DE Human; tumour related apoptosis inducing ligand; Trail;
 KW Trail prokaryotic expression system; tumour cell death.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Misc-difference 217
 FT /note= "Encoded by CTT"
 FT
 XX CN1354183-A.
 PN 19-JUN-2002.
 PD

XX 30-NOV-2001; 2001CN-00132371.
 XX 30-NOV-2001; 2001CN-00132371.
 PR (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
 XX Hu Y, Yao Y;
 XX WPI; 2002-751439/82.
 DR N-PSDB; ABX14391.
 XX Tumor death induction ligand gene, gene expression protein and its
 PT preparation method.
 PS Claim 7; Page 10 (disclosure); 17pp; Chinese.
 XX The present invention relates to the isolation of cDNA encoding human
 CC tumour related apoptosis inducing ligand (Trail), and the Trail protein.
 CC The Trail full length cDNA is cloned, and is utilised to create a Trail
 CC prokaryotic expression system. The full length Trail cDNA is used to
 CC respectively clone cDNA of soluble ectocytic segment Trail109 and Trail
 CC 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic
 CC expression systems. The prokaryotic expression systems created greatly
 CC increase the expression and quantity of the Trail, Trail109, and Trail114
 CC proteins, and may be useful in a new preparation for killing tumour
 CC cells. The present sequence represents the full length human Trail
 CC protein
 XX Sequence 281 AA;
 SQ

Query Match 70.8%; Score 199; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.3e-186;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DSDYDNDPNDDESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
 DB 61 DSDYDNDPNDDESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 QY 181 FYIYISQTYFRFQBEIKEN 199
 DB 181 FYIYISQTYFRFQBEIKEN 199

RESULT 55
 AAU99301
 ID AAU99301 standard; protein; 212 AA.
 XX AC AAU99301;
 XX DT 24-SEP-2002 (first entry)
 XX Human TRAIL splice variant 8, rpl-6-6, protein.
 DE Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
 KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
 KW TRAIL; apoptosis; programmed cell death; differentiation; development;
 KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
 KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
 KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
 KW chromosome 3q26; rpl-6-6.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH

FT	Domain	1. .16	/note= "Cytoplasmic domain"	Db	1	MAMMEVQGPSLGTCLVLIIVFTVLLQSLCVAVTVYFTTNELKQMDKYSKSGIACFLKE	60
FT	Domain	17. .38	/note= "Transmembrane domain"	Qy	61	DDSYDNDDESNMSPQWQVQLRQLVRRKMLRTSETISTVQEKQONISPLVRERGPO	120
FT	Domain	39. .212	/note= "Extracellular domain"	Db	61	DDSYDNDDESNMSPQWQVQLRQLVRRKMLRTSETISTVQEKQONISPLVRERGPO	120
FT	Misc-difference	209	/note= "Encoded by in-frame stop codon"	Qy	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG	180
FT				Db	121	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG	180
XX	US2002061525-A1.			Qy	181	FYIYSQTYFRFQ	193
XX	23-MAY-2002.			Db	181	FYIYSQTYFRFQ	193
XX	16-MAY-2001; 2001US-00855544.			RESULT 56			
XX	16-MAY-2000; 2000IL-00136156.			AAE11037			
XX	(YELI/) YELIN R.			ID	AAE11037	standard; protein; 253 AA.	
XX	(KHOS/) KHOSRAVI R.			XX	AC	AAE11037;	
XX	(SAVI/) SAVITZKY K.			XX	DT	18-DEC-2001 (first entry)	
XX	Yelin R, Khosravi R, Savitzky K;			XX	DE	GH-derived leader peptide-leucine zipper-human TRAIL fusion protein.	
XX	WPI; 2002-479259/51.			XX	KW	Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;	
XX	New splice variants of tumor necrosis factor-related apoptosis inducing			XX	KW	TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;	
XX	ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat			XX	KW	human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;	
XX	diseases or disorders associated with low expression of the variants.			XX	KW	melanoma; growth hormone; GH; leucine zipper; fusion protein;	
XX	Claim 4; Fig 8; 29pp; English.			XX	OS	chimeric protein.	
XX	The invention discloses isolated, naturally occurring, polypeptide splice			OS	OS	Homo sapiens.	
XX	variants of human tumour necrosis factor (TNF)-related apoptosis inducing			OS	OS	Unidentified.	
XX	ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal			XX	PH	Chimeric.	
XX	cellular differentiation and development of multicellular organisms.			XX	FT	Key	
XX	Apoptosis is induced by certain cytokines which include TNF and TRAIL			FT	Region	Location/Qualifiers	
XX	(also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane			FT	Region	1. .26	
XX	protein which induces apoptosis and nuclear factor-B (NF-B) activation in			FT	Region	/note= "GH-derived leader peptide"	
XX	many tissues and cells. Receptors for TRAIL include two death domain			FT	Region	27. .29	
XX	containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1			FT	Region	/note= "Tripeptide corresponding to an oligonucleotide	
XX	and DcR2, lacking the intracellular signalling death domain. TRAIL,			FT	Region	employed in vector construction"	
XX	induced by type I interferons, induces apoptosis in tumour cells, whereas			FT	Region	30. .63	
XX	normal cells are relatively resistant without showing significant toxic			FT	Region	/note= "Leucine zipper peptide"	
XX	side effects. Thus, TRAIL has the potential to be a very useful			FT	Region	64. .66	
XX	antitumour agent. The naturally occurring splice variants may differ in			FT	Region	/note= "Tripeptide corresponding to an oligonucleotide	
XX	their cellular distribution, expression levels/timing and activity.			FT	Region	employed in vector construction"	
XX	Determining these factors could provide possible mechanisms for the			FT	Region	67. .253	
XX	induction of apoptosis of tumours cells. The splice variant polypeptides			FT	Region	/note= "Human TRAIL protein fragment"	
XX	and polynucleotides can be used in gene therapy, to raise antibodies, to			XX	PN	US6284236-B1.	
XX	detect the levels, distribution and ratios of expression of TRAIL, and			XX	PD	04-SEP-2001.	
XX	its splice variants, in a biological sample and to identify compounds			XX	PF	26-MAY-1999; 99US-00320424.	
XX	which bind the variant TRAIL products and modulate its activity (agonists			XX	PR	29-JUN-1995; 95US-00496632.	
XX	and antagonists). Pharmaceutical compositions, comprising an expression			XX	PR	01-NOV-1995; 95US-00548368.	
XX	vector or any of the amino acid sequences, are useful for causing a			XX	PR	25-JUN-1996; 96US-00670354.	
XX	cytotoxic effect in cancer cells and for treatment of diseases which can			XX	PR	26-MAR-1998; 98US-00048641.	
XX	be ameliorated, cured or prevented by lowering or raising the level of			XX	PR	10-NOV-1998; 98US-00190046.	
XX	the amino acid sequences. The antibodies may also have a therapeutic			XX	PA	(IMMV) IMMUNEX CORP.	
XX	utility in blocking or decreasing the activity of the TRAIL variant			XX	PI	Wiley SR, Goodwin RG;	
XX	products. Diseases that may be treated include cancer, neurodegenerative			XX	PI	WPI; 2001-595463/67.	
XX	diseases, autoimmune diseases, diseases involved in the non-normal			XX	DR	N-PSDB; AAD18398.	
XX	development of tissues and aging. TRAIL's gene is located on chromosome			XX	DR		
XX	3q26. The sequence presented is the human TNF-related apoptosis inducing			XX	PT	New tumor necrosis factor related apoptosis inducing ligand polypeptides	
XX	ligand (TRAIL) splice variant 8, rpl-6-5, protein which has had an C-			XX	PT	for treating viral infections (e.g. bovine viral diarrhoea or human	
XX	terminal section of the conserved TNF domain deleted			XX	PT	immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).	
XX	Sequence 212 AA;			XX	PS	Claim 18; Fig 3; 41pp; English.	
XX	Query Match	68.7%;	Score 193; DB 5; Length 212;				
XX	Best Local Similarity	100.0%;	Pred. No. 2e-180;				
XX	Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	MAMMEVQGPSLGTCLVLIIVFTVLLQSLCVAVTVYFTTNELKQMDKYSKSGIACFLKE	60				

XX The invention relates to a cytokine designated as tumour necrosis factor
 CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
 CC of certain target cells, including cancer cells and virally infected
 CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
 CC treating viral infections (e.g. bovine viral diarrhoea or human
 CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
 CC melanoma), as a research reagent useful in studying apoptosis including
 CC the regulation of programmed cell death. TRAIL DNA sequences may be
 CC employed in developing a gene therapy approach to treating disorders
 CC mediated by defective or insufficient amounts of TRAIL, in the production
 CC of TRAIL polypeptides and as probes or primers in polymerase chain
 CC reactions (PCR). The present sequence is growth hormone (GH)-derived
 CC leader peptide-leucine zipper-human TRAIL fusion protein
 XX Sequence 253 AA;

Query Match 66.5%; Score 187; DB 4; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.7e-174;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVREGRGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSW 154
 DB 67 TSEETISTVQEKQONISPLVREGRGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSW 126

QY 155 ESSRSGHSFLSNLHNLNGELVIHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQIYKYT 214
 DB 127 ESSRSGHSFLSNLHNLNGELVIHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQIYKYT 186

QY 215 SYPPDPILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
 DB 187 SYPPDPILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246

QY 275 FGAFVLVG 281
 DB 247 FGAFVLVG 253

RESULT 57
 ABU08564
 ID ABU08564 standard; protein; 253 AA.
 AC ABU08564;
 XX
 DI 05-JUN-2003 (first entry)
 XX Human Growth hormone/leucine zipper/TRAIL 95-281 fusion protein.
 DE
 XX Human; TNF related apoptosis inducing ligand; TRAIL;
 KW tumour necrosis factor; apoptosis; haemostatic; immunosuppressive;
 KW antiinflammatory; dermatological; thrombotic microangiopathy;
 KW thrombotic thrombocytopenic purpura; TTP; HUS; SLE; clotting disorder;
 KW adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS;
 KW systemic lupus erythematosus; growth hormone; leucine zipper.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS Unidentified.
 XX
 PN US521228-B1.
 XX
 PD 18-FEB-2003.
 XX
 XX 02-APR-2001; 2001US-00825563.
 PF
 XX 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548368.
 PR 25-JUN-1996; 96US-00670354.
 PR 26-MAR-1998; 98US-00048641.
 PR 10-NOV-1998; 98US-00190046.
 PR 26-MAY-1999; 99US-00320424.
 XX
 PA (IMM) IMMUNEX CORP.

XX Willey SR, Goodwin RG;
 PI
 XX WPI; 2003-340628/32.
 DR N-FSDB; ABX93872.
 XX
 PT Novel antibody which binds to human tumor necrosis factor related
 PT apoptosis inducing ligand protein, useful for inhibiting TRAIL-mediated
 PT apoptosis of a target cell, or blocking binding of TRAIL to a target
 PT cell.
 XX
 PS Disclosure; Fig 3; 40pp; English.
 XX
 CC The invention relates to an antibody that specifically binds: (a) the
 CC human tumor necrosis factor (TNF) related apoptosis inducing ligand
 CC (TRAIL) protein appearing as ABU08558; (b) a soluble human TRAIL
 CC polypeptide; (c) a polypeptide comprising amino acids 124-276 of
 CC ABU08558, or (d) a fragment of the TRAIL protein. Also included is an
 CC antigen-binding fragment of the antibody (a monoclonal antibody), a
 CC hybridoma cell line that produces the antibody. The antibody is used in
 CC assays to detect the presence of TRAIL polypeptides, either in vitro or
 CC in vivo, purifying TRAIL by affinity chromatography, blocking binding of
 CC TRAIL to target cells and thus inhibiting a biological activity of TRAIL.
 CC The antibody is useful for treating disorders mediated or exacerbated by
 CC TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic
 CC thrombocytopenic purpura (TTP), adult haemolytic uraemic syndrome (HUS)
 CC (even though it can strike children as well) small blood vessel clotting
 CC disorders e.g., cardiac problems in paediatric AIDS patients and systemic
 CC lupus erythematosus (SLE). The present sequence represents a Growth
 CC hormone signal peptide/leucine zipper/TRAIL 95-281 fusion protein
 XX Sequence 253 AA;

Query Match 66.5%; Score 187; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.7e-174;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVREGRGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSW 154
 DB 67 TSEETISTVQEKQONISPLVREGRGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSW 126

QY 155 ESSRSGHSFLSNLHNLNGELVIHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQIYKYT 214
 DB 127 ESSRSGHSFLSNLHNLNGELVIHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQIYKYT 186

QY 215 SYPPDPILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
 DB 187 SYPPDPILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246

QY 275 FGAFVLVG 281
 DB 247 FGAFVLVG 253

RESULT 58
 AAE11038
 ID AAE11038 standard; protein; 256 AA.
 XX
 AC AAE11038;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE CMV-derived leader peptide-leucine zipper-human TRAIL fusion protein.
 XX
 KW Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
 KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
 KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
 KW melanoma; cytomegalovirus; CMV; leucine zipper; fusion protein;
 KW chimeric protein.
 XX
 OS Homo sapiens.
 OS Cytomegalovirus.
 OS Unidentified.

OS XX Chimeric.

PH Key Location/Qualifiers

FT Region 1. .29

FT Region 30. .32

FT Region /note= "CMV-derived leader peptide"

FT Region /note= "Triptide corresponding to an oligonucleotide employed in vector construction"

FT Region 33. .66

FT Region /note= "Leucine zipper peptide"

FT Region 67. .69

FT Region /note= "Triptide corresponding to an oligonucleotide employed in vector construction"

FT Region 70. .256

FT Region /note= "Human TRAIL protein fragment"

XX US6284236-B1.

XX 04-SEP-2001.

XX 26-MAY-1999; 99US-00320424.

XX 29-JUN-1995; 95US-00496632.

XX 01-NOV-1995; 95US-00548368.

XX 25-JUN-1996; 96US-00670354.

XX 26-MAR-1998; 98US-00048641.

XX 10-NOV-1998; 98US-00190046.

XX (IMMV) IMMUNEX CORP.

XX Wiley SR, Goodwin RG;

XX WPI; 2001-595463/67.

XX N-PSDB; AAD18399.

XX New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhoea or human immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).

XX Claim 20; Fig 4; 41pp; English.

XX The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in treating viral infections (e.g. bovine viral diarrhoea or human immunodeficiency virus (HIV) and cancers (e.g. leukaemia, lymphoma and melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polypeptides and as probes or primers in polymerase chain reactions (PCR). The present sequence is a DNA encoding cytomegalovirus (CMV)-derived leader peptide-leucine zipper-human TRAIL fusion protein

XX Sequence 256 AA;

Query Match 66.5%; Score 187; DB 4; Length 256;

Best Local Similarity 100.0%; Pred. No. 1.7e-174;

Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSEETISTVQKQNIPLVREGRQVAAHITGRGRNTLSSPNSKNEKALGRKINSW 154

Db 70 TSEETISTVQKQNIPLVREGRQVAAHITGRGRNTLSSPNSKNEKALGRKINSW 129

Qy 155 ESSRSGHSFLNLHRLNGELVIEHKGFFYYISQTYFRQBEIKENTKDKQWQYIYKYT 214

Db 130 ESSRSGHSFLNLHRLNGELVIEHKGFFYYISQTYFRQBEIKENTKDKQWQYIYKYT 189

Qy 215 SYDPDILLMSARNCSWKSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274

Db 190 SYDPDILLMSARNCSWKSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249

Qy 275 FGAPLVG 281

Db 250 FGAPLVG 256

RESULT 59

ABU08565

ID ABU08565 standard; protein; 256 AA.

XX AC ABU08565;

XX 05-JUN-2003 (first entry)

DT CMV sig. pep./leucine zipper/TRAIL 95-281 fusion protein.

DE Human; TNF related apoptosis inducing ligand; TRAIL; CMV;

XX tumour necrosis factor; apoptosis; haemostatic; immunosuppressive;

XX antiinflammatory; dermatological; thrombotic microangiopathy;

XX thrombotic thrombocytopenic purpura; TTP; HUS; SLE; clotting disorder;

XX adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS;

XX systemic lupus erythematosus; leucine zipper.

XX Homo sapiens.

OS Human Cytomegalovirus.

OS Unidentified.

OS Chimeric.

XX US6521228-B1.

XX 18-FEB-2003.

XX 02-APR-2001; 2001US-00825563.

XX 29-JUN-1995; 95US-00496632.

XX 01-NOV-1995; 95US-00548368.

XX 25-JUN-1996; 96US-00670354.

XX 26-MAR-1998; 98US-00048641.

XX 10-NOV-1998; 98US-00190046.

XX 26-MAY-1999; 99US-00320424.

XX (IMMV) IMMUNEX CORP.

XX Wiley SR, Goodwin RG;

XX WPI; 2003-340628/32.

XX N-PSDB; ABX3873.

XX Novel antibody which binds to human tumor necrosis factor related apoptosis inducing ligand protein, useful for inhibiting TRAIL-mediated apoptosis of a target cell, or blocking binding of TRAIL to a target cell.

XX Disclosure; Fig 4; 40pp; English.

XX The invention relates to an antibody that specifically binds: (a) the human tumor necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) protein appearing as ABU08558; (b) a soluble human TRAIL polypeptide; (c) a polypeptide comprising amino acids 124-276 of ABU08558; or (d) a fragment of the TRAIL protein. Also included is an antigen-binding fragment of the antibody (a monoclonal antibody), a hybridoma cell line that produces the antibody. The antibody is used in assays to detect the presence of TRAIL polypeptides. The antibody is used in vivo, to target cells by affinity chromatography, blocking binding of TRAIL to target cells and thus inhibiting a biological activity of TRAIL. The antibody is useful for treating disorders mediated or exacerbated by TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic thrombocytopenic purpura (TTP), adult haemolytic uraemic syndrome (HUS) (even though it can strike children as well) small blood vessel clotting disorders e.g., cardiac problems in paediatric AIDS patients and systemic lupus erythematosus (SLE). The present sequence represents a CMV (human cytomegalovirus) signal peptide/leucine zipper/TRAIL 95-281 fusion protein

SQ Sequence 256 AA;

Query Match 66.5%; Score 187; DB 6; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.7e-174;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVREGRGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 154
 DB 70 TSEETISTVQEKQONISPLVREGRGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 129
 QY 155 ESSRSCHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYT 214
 DB 130 ESSRSCHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYT 189
 QY 215 SYDPDILLMKSARNSCWSDAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
 DB 190 SYDPDILLMKSARNSCWSDAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249
 QY 275 FGAFLVG 281
 DB 250 FGAFLVG 256

RESULT 60
 AAO17496
 ID AAO17496 standard; protein; 461 AA.
 AC AAO17496;
 DT 11-JUL-2002 (first entry)
 DE Antibody-cytokine fusion protein #3.
 KW Antibody-cytokine fusion protein; proapoptotic; immunomodulatory; cancer;
 KW immune disease; multiple sclerosis; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antirheumatic; antiarthritic; antibacterial; virucide;
 KW protozoacide; antiallergic; antidiabetic; diabetes; infection;
 KW inflammation.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Region /note= "signal peptide"
 FT Region 20..267
 FT Region /note= "ScFv antibody fragment"
 FT Region 268..274
 FT Region /note= "linker peptide"
 FT Region 275..461
 FT Region /note= "immunoglobulin CH3 domain"
 FT Region 419..427
 FT Region /note= "linker peptide"
 FT Region 428..614
 FT /note= "human TRAIL protein fragment"
 PN WO200222680-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-EP010364.
 XX
 PR 15-SEP-2000; 2000DE-01045591.
 XX
 PA (PFIZ/) PFIZENWATER K.
 PA (WAJA/) WAJANT H.
 XX
 PI Pfizenmaier K, Wajant H, Moosmayer D, Wuest T;
 XX
 DR WPI: 2002-362336/39.
 DR N-PSDB; AAL46272.
 XX
 PT New polypeptide prodrug, useful e.g. for treating tumors, comprises
 PT cytokine, oligomerization domain and antibody specific for cytokine

PT receptor.
 XX
 PS Disclosure; Page 38-39; 45pp; German.
 XX
 CC The present invention relates to proteins comprising a segment with
 CC biological activity for a specific target molecule, a peptide linker, and
 CC a segment that is an antibody (or fragment) that recognises a specific
 CC target molecule on a cell surface. In absence of site-specific and/or
 CC selective binding of the antibody to the target, the biologically active
 CC segment has no biological activity. The proteins are useful in the
 CC treatment of cancers, infections (bacterial, viral or protozoal),
 CC metabolic diseases, inflammatory states (including allergy and transplant
 CC rejection), and autoimmune diseases, especially rheumatic/arthritic
 CC diseases but also multiple sclerosis and diabetes. The present sequence
 CC is a fusion protein of the invention
 XX
 SQ Sequence 461 AA;

Query Match 66.5%; Score 187; DB 5; Length 461;
 Best Local Similarity 100.0%; Pred. No. 2.7e-174;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVREGRGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 154
 DB 275 TSEETISTVQEKQONISPLVREGRGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 334
 QY 155 ESSRSCHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYT 214
 DB 335 ESSRSCHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYT 394
 QY 215 SYDPDILLMKSARNSCWSDAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
 DB 395 SYDPDILLMKSARNSCWSDAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 454
 QY 275 FGAFLVG 281
 DB 455 FGAFLVG 461

RESULT 61
 AAO17495
 ID AAO17495 standard; protein; 480 AA.
 XX
 AC AAO17495;
 DT 11-JUL-2002 (first entry)
 DE Antibody-cytokine fusion protein #2.
 XX
 KW Antibody-cytokine fusion protein; proapoptotic; immunomodulatory; cancer;
 KW immune disease; multiple sclerosis; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antirheumatic; antiarthritic; antibacterial; virucide;
 KW protozoacide; antiallergic; antidiabetic; diabetes; infection;
 KW inflammation.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Region /note= "signal peptide"
 FT Region 20..274
 FT Region /note= "ScFv antibody fragment"
 FT Region 275..293
 FT Region /note= "linker peptide"
 FT Region 294..480
 FT /note= "human TRAIL protein fragment"
 PN WO200222680-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-EP010364.
 XX

DT 14-FEB-2001 (first entry)
DE FC-huAGP-1 (95-281) fusion protein.
XX Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
KW transplant rejection; cardiovascular disease; arteriosclerosis;
KW FC-huAGP-1; fusion protein.
XX Homo sapiens.
OS WO200063253-A1.
FN 26-OCT-2000.
XX 24-MAR-2000; 2000WO-US008004.
PF 16-APR-1999; 99US-00293245.
XX (AMGE-) AMGEN INC.
PA Hsu H, Meng S;
XX WPI: 2000-665240/64.
DR N-PSDB; AAC67832.
XX Fusion protein of AGP-1 protein and an Fc region, used to treat
PT proliferative disorders, immune disorders, and virally-induced disorders.
PI Disclosure; Fig 3; 93pp; English.
PS The present sequence is an AGP-1 fusion protein. AGP-1 is a type II
XX transmembrane protein. The fusion proteins comprise an Fc immunoglobulin
CC region fused to the N-terminal portion of the AGP-1 protein. The fusion
CC proteins can be used to induce apoptosis in a tissue, and to treat
CC proliferative disorders, immune disorders, or virally-induced disorders.
CC The proliferative disorders include cancers, such as breast, prostate,
CC lung or colon cancer. The viral infections include hepatitis, and
CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion
CC proteins have increased biological activity compared to the soluble AGP-1
CC proteins used in prior art therapies
XX Sequence 441 AA;
SQ Query Match 66.2%; Score 186; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 2.5e-173; Mismatches 0; Indels 0; Gaps 0;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 95 TSEETISTVQEQQNISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
Db |||||||
256 TSEETISTVQEQQNISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 315
QY 155 ESSRSGHFLNLHURNGELVTHEGFFYIYSQTYFRQEEIKENTKNDKQWQVIYKYT 214
Db |||||||
316 ESSRSGHFLNLHURNGELVTHEGFFYIYSQTYFRQEEIKENTKNDKQWQVIYKYT 375
QY 215 SYDPDILLMKMSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db |||||||
275 FGAFLV 280
QY 436 FGAFLV 441
Db |||||||
RESULT 64
ADB61476
ID ADB61476 standard; protein; 281 AA.
XX

AC ADB61476;
XX 04-DEC-2003 (first entry)
XX Human Apo-2 ligand protein mutant S96C.
DE Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
XX high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW human; mutant; mutin.
XX Synthetic.
OS Homo sapiens.
FN Key Location/Qualifiers
XX Misc-difference 96 /note= "Native residue of Ser is substituted by Cys"
FT WO2003029420-A2.
XX 10-APR-2003.
XX 01-OCT-2002; 2002WO-US031210.
XX 02-OCT-2001; 2001US-0326622P.
XX (GETH) GENENTECH INC.
PI Kelley RF, Lindstrom SH;
XX WPI: 2003-541400/51.
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
PT cancer or an immune-related disease such as multiple sclerosis, comprises
PT amino acid substitutions in the native sequence of the Apo-2 ligand.
XX Claim 1; Page; 92pp; English.
XX The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide having a sequence that differs from the native sequence
CC having 281 amino acids given in specification. The Apo-2 ligand variant
CC polypeptide is selected from a polypeptide having substitutions at
CC residue positions identified from x-ray crystal structure of the
CC DR5.Apo2L complex. The polypeptide having the substitutions made at
CC residue position(s) selected from 20 positions such as S96C, S101C,
CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
CC residue position is, outside of the receptor contact region of the
CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
CC and further compositions have the following activities: cytostatic,
CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
CC inducing apoptosis in mammalian cells, by exposing mammalian cells
CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
CC immune-related disease (such as arthritis or multiple sclerosis) in a
CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the human Apo-2 ligand mutant S96C
CC protein of the invention. NOTE: This sequence is not shown in the
CC specification. It has been created from information provided in claim 1
CC and from the sequence in Fig 1 of the specification.
XX Sequence 281 AA;
SQ Query Match 65.8%; Score 185; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.7e-172;

PF 01-OCT-2002; 2002WO-US031210.
XX ADB61484
PR 02-OCT-2001; 2001US-0326622P.
XX ADB61484 standard; protein; 281 AA.
PA (GETH) GENENTECH INC.
XX
PI Kelley RF, Lindstrom SH;
XX
DR WPI; 2003-541400/51.
XX
PT Novel isolated Apo-2 ligand variant polypeptide useful for treating
PT cancer or an immune-related disease such as multiple sclerosis, comprises
PT amino acid substitutions in the native sequence of the Apo-2 ligand.
XX
PS Claim 1; Page; 92pp; English.
XX
CC The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide having a sequence that differs from the native sequence
CC having 281 amino acids given in specification. The Apo-2 ligand variant
CC polypeptide is selected from a polypeptide having substitutions at
CC residue positions identified from x-ray crystal structure of the
CC DR5.Apo2L complex. The polypeptide having the substitutions made at
CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
CC residue position is, outside of the receptor contact region of the
CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
CC and further compositions have the following activities: cytostatic,
CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
CC inducing apoptosis in mammalian cells, by exposing mammalian cells
CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
CC immune-related disease (such as arthritis or multiple sclerosis) in a
CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the human Apo-2 ligand mutant E144C
CC protein of the invention. NOTE: This sequence is not shown in the
CC specification. It has been created from information provided in claim 1
CC and from the sequence in Fig 1 of the specification.
XX
SQ Sequence 281 AA;
Query Match
Best Local Similarity 64.1%; Score 180; DB 7; Length 281;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTLLQSLCAVTVVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTLLQSLCAVTVVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQWQLPOLVKRMILRTSEETISTVQEKQONISPLVRGPQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWQLPOLVKRMILRTSEETISTVQEKQONISPLVRGPQ 120
QY 121 RVAAHITGRGNTLSSPNSKNEALGRKINSWESSRSGHSFLSNLHRLNGELVHKG 180
Db 121 RVAAHITGRGNTLSSPNSKNEALGRKINSWESSRSGHSFLSNLHRLNGELVHKG 180
QY 181 FYIYSQYFRQBEIKENTKNDKQVQYKYTSYDPDILMLKSGARNSCKWDAEYGLY 240
Db 181 FYIYSQYFRQBEIKENTKNDKQVQYKYTSYDPDILMLKSGARNSCKWDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFVNG 281
Db 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFVNG 281

RESULT 67
ADB61484
ID ADB61484 standard; protein; 281 AA.
XX
AC ADB61484;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human Apo-2 ligand protein mutant E144C.
XX
KW Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW human; mutant; mutein.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 114 /note= "Native residue of Glu is substituted by Cys"
XX
XX WO2003029420-A2.
XX
XX 10-APR-2003.
XX
XX 01-OCT-2002; 2002WO-US031210.
XX
XX 02-OCT-2001; 2001US-0326622P.
XX (GETH) GENENTECH INC.
XX Kelley RF, Lindstrom SH;
XX WPI; 2003-541400/51.
XX
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
XX cancer or an immune-related disease such as multiple sclerosis, comprises
XX amino acid substitutions in the native sequence of the Apo-2 ligand.
XX
XX Claim 1; Page; 92pp; English.
XX
XX The invention relates to a novel isolated Apo-2 ligand variant
XX polypeptide having a sequence that differs from the native sequence
XX having 281 amino acids given in specification. The Apo-2 ligand variant
XX polypeptide is selected from a polypeptide having substitutions at
XX residue positions identified from x-ray crystal structure of the
XX DR5.Apo2L complex. The polypeptide having the substitutions made at
XX S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
XX R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
XX residue position is, outside of the receptor contact region of the
XX DR5.Apo2L complex, and displays high solvent accessibility in the crystal
XX structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
XX and further compositions have the following activities: cytostatic,
XX antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
XX an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
XX inducing apoptosis in mammalian cells, by exposing mammalian cells
XX expressing a receptor selected from DR4 receptor and DR5 receptor to a
XX therapeutically effective amount of the Apo-2 ligand variant polypeptide,
XX Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
XX colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
XX the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
XX treating cancer (such as lung, breast, colon or colorectal cancer) or an
XX immune-related disease (such as arthritis or multiple sclerosis) in a
XX mammal, by administering to the mammal an effective amount of the Apo-2
XX ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
XX trimer. This sequence represents the human Apo-2 ligand mutant N134C
XX protein of the invention. NOTE: This sequence is not shown in the
XX specification. It has been created from information provided in claim 1
XX and from the sequence in Fig 1 of the specification.
XX

SQ Sequence 281 AA;
 Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDNDESMNSPCWQKWLRLVRKMLTSETISTVQEKQNTISPLVRERGPO 120
 DB 61 DDSYWDNDESMNSPCWQKWLRLVRKMLTSETISTVQEKQNTISPLVRERGPO 120
 QY 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 DB 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 68
 ADB61478
 ID ADB61478 standard; protein; 281 AA.
 AC ADB61478;
 XX 04-DEC-2003 (first entry)
 DT Human Apo-2 ligand protein mutant S111C.
 DE
 XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX Synthetic.
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 111
 FT /note= "Native residue of Ser is substituted by Cys"
 FT
 XX WO2003029420-A2.
 XX 10-APR-2003.
 XX 01-OCT-2002; 2002WO-US031210.
 XX 02-OCT-2001; 2001US-0326622P.
 XX (GETH) GENENTECH INC.
 XX Kelley RF, Lindstrom SH;
 XX WPI; 2003-541400/51.
 XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
 FT cancer or an immune-related disease such as multiple sclerosis, comprises
 FT amino acid substitutions in the native sequence of the Apo-2 ligand.
 XX
 PS Claim 1; Page; 92pp; English.
 CC The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant

polypeptide is selected from a polypeptide having substitutions at
 residue positions identified from x-ray crystal structure of the
 DR5.Apo2L complex. The polypeptide having the substitutions made at
 residue position(s) selected from 20 positions such as S96C, S101C,
 S111C, V114C, E115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
 R170K, R170S, K179C, D234C, E249C, R259C, E263C, H264C, such that the
 residue position is, outside of the receptor contact region of the
 DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 and further compositions have the following activities: cytostatic,
 antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 inducing apoptosis in mammalian cells, by exposing mammalian cells
 expressing a receptor selected from DR4 receptor and DR5 receptor to a
 therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 treating cancer (such as lung, breast, colon or colorectal cancer) or an
 immune-related disease (such as arthritis or multiple sclerosis) in a
 mammal, by administering to the mammal an effective amount of the Apo-2
 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 trimer. This sequence represents the human Apo-2 ligand mutant S111C
 protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.
 XX
 SQ Sequence 281 AA;
 Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDNDESMNSPCWQKWLRLVRKMLTSETISTVQEKQNTISPLVRERGPO 120
 DB 61 DDSYWDNDESMNSPCWQKWLRLVRKMLTSETISTVQEKQNTISPLVRERGPO 120
 QY 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 DB 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 69
 ADB61481
 ID ADB61481 standard; protein; 281 AA.
 AC ADB61481;
 XX 04-DEC-2003 (first entry)
 DT Human Apo-2 ligand protein mutant E116C.
 DE
 XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX Synthetic.
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Misc-difference 116 /note= "Native residue of Glu is substituted by Cys"
 FT XX WO2003029420-A2.
 PN 10-APR-2003.
 PD XX
 XX
 PF 01-OCT-2002; 2002WO-US031210.
 XX
 PR 02-OCT-2001; 2001US-0326622P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Kelley RF, Lindstrom SH;
 PI WPI; 2003-541400/51.
 XX
 DR Novel isolated Apo-2 ligand variant polypeptide useful for treating
 XX cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.
 PT
 XX
 PS Claim 1; Page; 92pp; English.
 XX
 CC The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 XX

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SQ Sequence 281 AA;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNELKOMQDKYSKGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNELKOMQDKYSKGIACFLKE 60
 QY 61 DDSYWDPNDESMNSPCWQVQWQLRQVLRKMLRTSEETISTVQVKQNI SPLVRGPQ 120
 DB 61 DDSYWDPNDESMNSPCWQVQWQLRQVLRKMLRTSEETISTVQVKQNI SPLVRGPQ 120
 QY 121 RVAAHITGRGRSNTLSSPNSKNEALGRKKNWSWESSRSGHSFSLNHLRNGELVIEHKG 180
 DB 121 RVAAHITGRGRSNTLSSPNSKNEALGRKKNWSWESSRSGHSFSLNHLRNGELVIEHKG 180
 QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDPDILLMKRSARNSCWSKDAEYGLY 240

Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDPDILLMKRSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLDMDEHSEAFSGAFLVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLDMDEHSEAFSGAFLVG 281
 RESULT 70
 ADB61487
 ID ADB61487 standard; protein; 281 AA.
 XX
 AC ADB61487;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human Apo-2 ligand protein mutant R170C.
 XX
 KW Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 170 /note= "Native residue of Arg is substituted by Cys"
 XX
 DN WO2003029420-A2.
 XX
 PD 10-APR-2003.
 XX
 XX 01-OCT-2002; 2002WO-US031210.
 XX
 PR 02-OCT-2001; 2001US-0326622P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Kelley RF, Lindstrom SH;
 XX WPI; 2003-541400/51.
 XX
 PT Novel isolated Apo-2 ligand variant polypeptide useful for treating
 PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.
 XX
 PS Claim 1; Page; 92pp; English.
 XX
 CC The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 XX

CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant R170C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.
 XX
 SQ Sequence 281 AA;

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGTQCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGTQCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESMNSPCWQVKWQLRQLVKMLTSETTSTVQEKQONISPLVREGPQ 120
 DB 61 DDSYWDPNDESMNSPCWQVKWQLRQLVKMLTSETTSTVQEKQONISPLVREGPQ 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 71
 ADB61485
 ID ADB61485 standard; protein; 281 AA.
 AC ADB61485;
 XX
 DT 04-DEC-2003 (first entry)
 XX Human Apo-2 ligand protein mutant N152C.
 DE
 XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH MISC-difference 152
 FT /note= "Native residue of Asn is substituted by Cys"
 FT
 XX WO2003029420-A2.
 PN
 XX 10-APR-2003.
 PD
 XX 01-OCT-2002; 2002WO-US031210.
 PF
 XX 02-OCT-2001; 2001US-032622P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Kelley RF, Lindstrom SH;
 PI WPT; 2003-541400/51.
 DR
 XX Novel isolated Apo-2 ligand variant polypeptide useful for treating

PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.

XX Claim 1; Page; 92pp; English.

XX
 CC The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, K179C, D234C, E249C, R255C, E264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytosolic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant N152C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.
 XX
 SQ Sequence 281 AA;

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGTQCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGTQCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESMNSPCWQVKWQLRQLVKMLTSETTSTVQEKQONISPLVREGPQ 120
 DB 61 DDSYWDPNDESMNSPCWQVKWQLRQLVKMLTSETTSTVQEKQONISPLVREGPQ 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 72
 ADB61490
 ID ADB61490 standard; protein; 281 AA.
 XX
 AC ADB61490;
 XX
 DT 04-DEC-2003 (first entry)
 XX Human Apo-2 ligand protein mutant K179C.
 DE
 XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;

high solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis; human; mutant; mutein.

Synthetic.
OS Homo sapiens.

Key Location/Qualifiers
FH Misc-difference 179 /note= "Native residue of Lys is substituted by Cys"
FT WO2003029420-A2.
FN 10-APR-2003.
PD 01-OCT-2002; 2002WO-US031210.
PF 02-OCT-2001; 2001US-0326622P.
PR (GETH) GENENTECH INC.
PA Kelley RF, Lindstrom SH;
PI WPI; 2003-541400/51.
PD Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
PS Claim 1; Page; 92pp; English.

The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DR5 Apo2L complex. The polypeptide having the substitutions made at residue position(s) selected from 20 positions such as S96C, S101C, S111C, V114C, R115C, E116C, N134C, E144C, N152C, S153C, R170C, R170K, R170S, K179C, D234C, E249C, R255C, E263C, such that the residue position is, outside of the receptor contact region of the DR5 Apo2L complex, and displays high solvent accessibility in the crystal structure of the DR5 Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide inducing apoptosis in mammalian cells, by exposing mammalian cells an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for expressing a receptor selected from DR4 receptor and DR5 receptor to a therapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for treating cancer (such as lung, breast, colon or colorectal cancer) or an immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the human Apo-2 ligand mutant K179C protein of the invention. NOTE: This sequence is not shown in the specification. It has been created from information provided in claim 1 and from the sequence in Fig 1 of the specification.

Query Match 64.11%; Score 180; DB 7; Length 281;
Best Local Similarity 99.6%; Pred. No. 1.3e-167;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQCVLIVITVLLQSLCAVAVTVYTNELKQMDKYSKSGTACFLKE 60
DB 1 MAMMEVQGGPSIGQCVLIVITVLLQSLCAVAVTVYTNELKQMDKYSKSGTACFLKE 60
QY 61 DDSYWDNDDESMNSPCWQVKWQLRQVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

Db 61 DDSYWDNDDESMNSPCWQVKWQLRQVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLANGELVIEHG 180
Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLANGELVIEHG 180
QY 181 FYIYSQTYFRFOBEIKENTKNDKQWQVYIKYKTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOBEIKENTKNDKQWQVYIKYKTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYOGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 73
ADB61477
ID ADB61477 standard; protein; 281 AA.
XX ADB61477;
XX 04-DEC-2003 (first entry)
XX Human Apo-2 ligand protein mutant S101C.
XX Apo-2 ligand; DR5 Apo2L complex; receptor contact region;
KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW human; mutant; mutein.
XX Synthetic.
OS Homo sapiens.

Key Location/Qualifiers
FH Misc-difference 101 /note= "Native residue of Ser is substituted by Cys"
FT WO2003029420-A2.
XX 10-APR-2003.
XX 01-OCT-2002; 2002WO-US031210.
XX 02-OCT-2001; 2001US-0326622P.
XX (GETH) GENENTECH INC.
XX Kelley RF, Lindstrom SH;
XX WPI; 2003-541400/51.
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
XX Claim 1; Page; 92pp; English.

The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DR5 Apo2L complex. The polypeptide having the substitutions made at residue position(s) selected from 20 positions such as S96C, S101C, S111C, V114C, R115C, E116C, N134C, E144C, N152C, S153C, R170C, R170K, R170S, K179C, D234C, E249C, R255C, E263C, such that the residue position is, outside of the receptor contact region of the DR5 Apo2L complex, and displays high solvent accessibility in the crystal structure of the DR5 Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide inducing apoptosis in mammalian cells, by exposing mammalian cells an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for expressing a receptor selected from DR4 receptor and DR5 receptor to a therapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for treating cancer (such as lung, breast, colon or colorectal cancer) or an immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the human Apo-2 ligand mutant K179C protein of the invention. NOTE: This sequence is not shown in the specification. It has been created from information provided in claim 1 and from the sequence in Fig 1 of the specification.

CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant S101C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.

XX Sequence 281 AA;

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.3e-167;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 TVQEKQNIPLVBERGQPVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGH 161
 DB 102 TVQEKQNIPLVBERGQPVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGH 161
 QY 162 SFLSNLHRLNGELVIHEKGFYIYSQYFRFQBEIKENTKNDKQWQYIYKTSYPPDIL 221
 DB 162 SFLSNLHRLNGELVIHEKGFYIYSQYFRFQBEIKENTKNDKQWQYIYKTSYPPDIL 221
 QY 222 LMKARNCSWKSQDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 222 LMKARNCSWKSQDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 74

ADB61479
 ID ADB61479 standard; protein; 281 AA.

XX ADB61479;

DT 04-DEC-2003 (first entry)

XX Human Apo-2 ligand protein mutant V114C.

XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Misc-difference 114 /note= "Native residue of Val is substituted by Cys"

FT WO2003029420-A2.

XX 10-APR-2003.

XX 01-OCT-2002; 2002WO-US031210.

XX 02-OCT-2001; 2001US-0326622P.

XX (GETH) GENENTECH INC.

XX Kelley RF, Lindstrom SH;

XX WPI; 2003-541400/51.

XX Novel isolated Apo-2 ligand variant polypeptide useful for treating

PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.

XX Claim 1; Page: 92pp; English.

XX The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, N144C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, K179C, D234C, E249C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant V114C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.

XX Sequence 281 AA;

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVYVYFTNELKQMDQKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVYVYFTNELKQMDQKYSKSGIACFLKE 60
 QY 61 DSDYWPNDDEESMNSPCWQVKQLRVLVRKMLRTSEETISTVQEKQNIPLVBERGPQ 120
 DB 61 DSDYWPNDDEESMNSPCWQVKQLRVLVRKMLRTSEETISTVQEKQNIPLVBERGPQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVHEKG 180
 QY 181 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKTSYPPDILLMKARNCSWKSQDAEYGLY 240
 DB 181 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKTSYPPDILLMKARNCSWKSQDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 75

ADB61486

ID ADB61486 standard; protein; 281 AA.

XX ADB61486;

XX 04-DEC-2003 (first entry)

XX Human Apo-2 ligand protein mutant S153C.

XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;

KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW human; mutant; mutin.

XX	
OS	Synthetic.
OS	Homo sapiens.

Homo sapiens.

Key	Location/Qualifiers
FH	
FH	

Misc-difference

FT	/note=	"Native residue of Ser is substituted by Cys"
----	--------	---

PN WO2003029420-A2.

10-APR-2003

XX
FD 10-AFK-2003:

01-OCT-2002: 2002WO-US031210-

02-0CT-2001: 2001US-03

XX PA (CETH) GENENTECH INC

XXII

XX

XX

PT cancer or an immune-related disease such as multiple sclerosis, comprises PT amino acid substitutions in the native sequence of the Apo-2 ligand.

XX
SQ Sequence 281 AA;

Query Match

Query Match 64.1%; Score 180; DB 7; Length 281;

Best Local Similarity 99.6%; Pred. No. 1.3e-167;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLI VIFTVLLQSLCVAVTYVYFTNELKOMODKYSKSGIACFLKE 60

100

DB	I	MAMMEVQGGPSLGGTCVLIVIFVTLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE	60
QY	61	DDSYWDPNDESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRRGGPO	120

61	DDSYWDPNDESSMPCWQVKWQLRQVVRKMIILRTSEETISTVQEQKQINISPLVRERPQ	120
121	RVAAHITCTGRSNTLSSPNSKNEKALGRKINQSWSSRGSHGFLSNLHLRNGELVIHEKG	180
121	RVAAHITCTGRSNTLSSPNSKNEKALGRKINQSWSSRGSHGFLSNLHLRNGELVIHEKG	180
181	FYIYSQYTFYFFQBEIKENTKNDQWQYIYKYKTSYDPDILLMKSNRSCSKDAEYGLY	240
181	FYIYSQYTFYFFQBEIKENTKNDQWQYIYKYKTSYDPDILLMKSNRSCSKDAEYGLY	240
241	SIYQGGIFELKENDRIFFVSVTNEHLIDMDHEA5FFGAFLVG	281
241	SIYQGGIFELKENDRIFFVSVTNEHLIDMDHEA5FFGAFLVG	281

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180

Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINCWESSRSGHSFLSNLHLRNGELVIEKG 180

QY 181 FYYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

D**b** 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Search completed: March 23, 2004, 09:22:12
Job time : 64 secs

Job time : 64 secs

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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:19:40 ; Search time 45 Seconds
(without alignments)
1970.236 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MAMMEVQGPSLQQTCLIV.....NEHLIDMDEASFGAFLVG 281

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	10.3	287	11	Q8K3G0
2	13	4.6	304	13	Q7T1F2
3	8	2.8	465	17	Q9HKC2
4	8	2.8	473	16	Q8FUC2
5	8	2.8	475	10	Q8S6N3
6	8	2.8	643	16	Q9RZ93
7	8	2.8	939	5	Q9NG57
8	8	2.8	950	5	O15788
9	8	2.8	1248	5	Q8IBZ8
10	7	2.5	39	5	Q95NV2
11	7	2.5	73	16	Q7URQ9
12	7	2.5	88	2	Q8KH11
13	7	2.5	92	3	Q870H0
14	7	2.5	93	17	Q9HSN3
15	7	2.5	94	16	Q8PMD7
16	7	2.5	106	10	Q9LV97

17	7	2.5	107	17	Q97Y77
18	7	2.5	112	16	Q932M3
19	7	2.5	121	16	Q7U9A5
20	7	2.5	125	2	P72087
21	7	2.5	134	5	Q8MM82
22	7	2.5	155	17	Q9YBC2
23	7	2.5	157	2	Q83TU1
24	7	2.5	172	5	Q9N8D4
25	7	2.5	193	16	Q8P7K6
26	7	2.5	204	16	Q82UJ6
27	7	2.5	216	16	Q8F1X9
28	7	2.5	217	10	Q8LTD0
29	7	2.5	220	16	Q89V44
30	7	2.5	222	16	Q8DFN8
31	7	2.5	231	5	P90611
32	7	2.5	247	2	Q9EZK4
33	7	2.5	247	16	Q99RD5
34	7	2.5	251	3	O94262
35	7	2.5	253	16	Q98D64
36	7	2.5	271	16	Q81WU0
37	7	2.5	293	11	Q8ROL0
38	7	2.5	296	16	Q823E7
39	7	2.5	298	16	Q8E3I3
40	7	2.5	298	16	Q8DXW4
41	7	2.5	318	4	Q96QL7
42	7	2.5	322	5	Q9VI33
43	7	2.5	327	16	Q9PEN6
44	7	2.5	329	16	Q9ZKY9
45	7	2.5	343	16	Q7YU23
46	7	2.5	354	16	Q84846
47	7	2.5	354	16	Q9FL80
48	7	2.5	359	10	Q9AVE6
49	7	2.5	361	13	Q98SU0
50	7	2.5	367	5	Q8WPJ2
51	7	2.5	374	16	Q7U3W6
52	7	2.5	375	16	Q9L5E1
53	7	2.5	375	17	Q8TWS8
54	7	2.5	379	16	Q89SW4
55	7	2.5	389	10	Q9LTH1
56	7	2.5	401	16	Q9PC23
57	7	2.5	401	16	Q87CC1
58	7	2.5	402	4	Q9H766
59	7	2.5	404	17	Q9UX27
60	7	2.5	406	16	Q99XN8
61	7	2.5	406	16	Q8NZ26
62	7	2.5	406	16	Q8K5J7
63	7	2.5	414	10	Q8S179
64	7	2.5	417	2	Q8KIU0
65	7	2.5	417	2	Q8KIR0
66	7	2.5	420	5	Q8I514
67	7	2.5	423	4	Q9NWF0
68	7	2.5	424	10	Q9ZV11
69	7	2.5	425	10	Q8LP64
70	7	2.5	427	16	Q83835
71	7	2.5	428	17	Q9HSA2
72	7	2.5	429	16	Q9Z913
73	7	2.5	435	11	Q80ZJ8
74	7	2.5	449	5	Q8SWZ1
75	7	2.5	457	16	Q7WQF5
76	7	2.5	457	16	Q7WCF0
77	7	2.5	462	12	Q7TBL2
78	7	2.5	462	12	Q7TBK8
79	7	2.5	462	16	Q8EHZ9
80	7	2.5	474	16	Q82GJ4
81	7	2.5	479	16	Q8PDL5
82	7	2.5	485	5	Q8LIE5
83	7	2.5	494	2	Q8RJJ0
84	7	2.5	494	2	Q8RN10
85	7	2.5	494	2	Q8RN18
86	7	2.5	494	2	Q8RN38
87	7	2.5	494	2	Q8RN13
88	7	2.5	494	2	Q8RN23
89	7	2.5	494	2	Q8RJ26

Q97Y77	sulfolobus
Q932M3	staphylococ
Q7U9A5	synecococc
P72087	neisseria m
Q8MM82	caenorhabdi
Q9YBC2	aeropyrum p
Q83TU1	staphylococ
Q9N8D4	trypanosoma
Q8P7K6	xanthomonas
Q82UJ6	nitrosomona
Q8F1X9	xanthomonas
Q8LTD0	arabidopsis
Q89V44	bradyrhizob
Q8DFN8	vibrio vuln
P90611	toxoplasma
Q9EZK4	staphylococ
Q99RD5	staphylococ
O94262	schizosacch
Q98D64	rhizobium l
Q81WU0	bacillus an
Q8ROL0	mus musculu
Q823E7	chlamydophi
Q8E3I3	streptococc
Q8DXW4	streptococc
Q96QL7	homo sapien
Q9VI33	drosofila
Q9PEN6	xyella fas
Q9ZKY9	helicobacte
Q7YU23	helicobacte
Q84846	chlamydia t
Q9FL80	chlamydia t
Q9AVE6	oryza sativ
Q98SU0	xenopus lae
Q8WPJ2	mytilus edu
Q7U3W6	synecococc
Q9L5E1	salmonella
Q8TWS8	methanopyru
Q89SW4	bradyrhizob
Q9LTH1	arabidopsis
Q9PC23	xyella fas
Q87CC1	xyella fas
Q9H766	homo sapien
Q9UX27	sulfolobus
Q99XN8	streptococc
Q8NZ26	streptococc
Q8K5J7	streptococc
Q8S179	oryza sativ
Q8KIU0	pseudomonas
Q8KIR0	pseudomonas
Q8I514	plasmodium
Q9NWF0	homo sapien
Q9ZV11	arabidopsis
Q8LP64	brassica de
Q83835	treponema p
Q9HSA2	halobacteri
Q9Z913	chlamydia p
Q80ZJ8	mus musculu
Q8SWZ1	drosofila
Q7WQF5	borderella
Q7WCF0	borderella
Q7TBL2	bovine ente
Q7TBK8	bovine ente
Q8EHZ9	shewanella
Q82GJ4	streptomyce
Q8PDL5	xanthomonas
Q8LIE5	plasmodium
Q8RJJ0	campylobact
Q8RN10	campylobact
Q8RN18	campylobact
Q8RN38	campylobact
Q8RN13	campylobact
Q8RN23	campylobact
Q8RJ26	campylobact

90 7 2.5 516 11 Q8C4C3 mus musculus
 91 7 2.5 519 11 Q8R4G2 mus musculus
 92 7 2.5 519 11 Q9J1L4 mus musculus
 93 7 2.5 519 11 Q9CQ72 mus musculus
 94 7 2.5 523 11 Q8CDP5 mus musculus
 95 7 2.5 549 16 Q8PQ15 xanthomonas
 96 7 2.5 565 16 Q8KTU6 oktus vibrio chol
 97 7 2.5 579 16 Q8RI43 oktus vibrio chol
 98 7 2.5 630 16 Q8EVG2 mycoplasma
 99 7 2.5 680 5 Q8WSN8 caenothabdi
 100 7 2.5 686 16 Q8ABC4 caenothabdi

ALIGNMENTS

RESULT 1
 Q8K3G0 PRELIMINARY; PRT; 287 AA.
 ID Q8K3G0;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE TNF-related apoptosis inducing ligand.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DA;
 RA "Rattus norvegicus TNF-related apoptosis inducing ligand (TRAIL).";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A115578; AAM4797.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF-like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 SQ SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;

Query Match 10.3%; Score 29; DB 11; Length 287;
 Best Local Similarity 100.0%; Pred. No. 1.7e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 KOMVQYVYKYTSYPDILLMKARNSCWS 232
 Db |||||

214 KOMVQYVYKYTSYPDILLMKARNSCWS 242

RESULT 2
 Q7T1F2 PRELIMINARY; PRT; 304 AA.
 ID Q7T1F2;
 AC Q7T1F2;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DE TNF-related apoptosis inducing ligand.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;
 RA "Identification and Characterization of Chicken TNF-Superfamily
 RT Ligand 8 (CD30 Ligand) and 10 (Tumor Necrosis Factor Related Apoptosis
 RT Inducing Ligand TRAIL).";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB114678; BAC79267.1; -.
 SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 4.6%; Score 13; DB 13; Length 304;
 Best Local Similarity 100.0%; Pred. No. 8.7e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 GFYIYISQTYPRF 192
 Db |||||

184 GFYIYISQTYPRF 196

RESULT 3
 Q8HKC2 PRELIMINARY; PRT; 465 AA.
 ID Q8HKC2;
 AC Q8HKC2;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE Hypothetical membrane protein.
 GN TA0679.
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 OC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=2303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE=20479972; PubMed=1029001;
 RA Rupp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
 RT acidophilum.";
 RL Nature 407:508-513 (2000).
 DR EMBL; AL445065; CAC11817.1; -.
 DR InterPro; IPR007272; DUF395.
 DR Pfam; PF04143; DUF395; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 465 AA; 51450 MW; 74E47FAFF0C44B5A CRC64;

Query Match 2.8%; Score 8; DB 17; Length 465;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 SFFGAFV 280
 Db |||||

402 SFFGAFV 409

RESULT 4
 Q8FUC2 PRELIMINARY; PRT; 473 AA.
 ID Q8FUC2;
 AC Q8FUC2;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE Conserved hypothetical protein.
 GN CE0098.
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=152794;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
 RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
 Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

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RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005214; BAC16908.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 473 AA; 52745 MW; 9BFBGD8D8AABE249 CRC64;

Query Match          2.8%; Score 8; DB 16; Length 473;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 LVRRGPQ 120
Db 366 LVRRGPQ 373

RESULT 5
Q8S6N3 PRELIMINARY; PRT; 475 AA.
AC Q8S6N3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative kelch-containing protein.
GN OSUNBA0073L01.3.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.V., Taitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann J., Hsiao J.J., Blunt S., Vanaken S.S.,
RA Uterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RA "Oryza sativa chromosome 10 BAC OSUNBA0073L01 genomic sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569 (2003).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092548; AAM18732.1; -.
DR EMBL; AE017083; AAP53323.1; -.
DR Gramene; Q8S6N3; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF01344; Kelch; 2.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00612; Kelch; 2.
DR PROSITE; PS0181; FBOX; 1.
SQ SEQUENCE 475 AA; 51606 MW; 84258271A075D2EE CRC64;

Query Match          2.8%; Score 8; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 LSSPNSKN 143
Db 5 LSSPNSKN 12

RA Ma C.L., Yu X.B., Shan Z.X., Li X.R.;
RT "Polymorphisms in the genes are linked to Chloroquine-Resistant

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RESULT 6
Q9RZ93 PRELIMINARY; PRT; 643 AA.
AC Q9RZ93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Drug transport protein, putative.
GN D8A0061.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577 (1999).
DR EMBL; AE001862; AAP12254.1; -.
DR FIR; G75599; G75599.
DR TIGR; D8A0061; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0015520; F: tetracycline:hydrogen antiporter activity; IEA.
DR GO; GO:0005215; F: transporter activity; IEA.
DR GO; GO:0015904; P: tetracycline transport; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR004638; Biflux_EmrB.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub transporter.
DR InterPro; IPR001958; TCR_TetA.
DR InterPro; IPR001411; TCR_TetB.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PRO1035; TCR_TET.
DR PRINTS; PRO1036; TCR_TETB.
DR TIGRFAMs; TIGR00711; efflux_EmrB; 1.
DR PROSITE; PS00850; MFS; 1.
KW Complete proteome.
SQ SEQUENCE 643 AA; 67778 MW; 4168A0998E467A63 CRC64;

Query Match          2.8%; Score 8; DB 16; Length 643;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 VLIIVFTV 24
Db 231 VLIIVFTV 238

RESULT 7
Q9NG57 PRELIMINARY; PRT; 939 AA.
AC Q9NG57;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CGI protein.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FCCL/HN;
RA Ma C.L., Yu X.B., Shan Z.X., Li X.R.;
RT "Polymorphisms in the genes are linked to Chloroquine-Resistant

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RT Plasmodium falciparum in China."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF260819; RAF69519.1; --
 DR InterPro: IPR009011; Man_6_P_R_bind.
 SQ SEQUENCE 939 AA; 109367 MW; EE96972DC096412D CRC64;

Query Match 2.8%; Score 8; DB 5; Length 939;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140
 DB 373 SNTLSSPN 380

RESULT 8

ID O15788 PRELIMINARY; PRT; 950 AA.
 AC O15788;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CGL.
 GN CGL.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1] _SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB3;
 RX MEDLINE=98054002; PubMed=9393853;
 RA Su X., Kirkman L.A., Fujioka H., Wellens T.E.;
 RT "Complex polymorphisms in an approximately kDa protein are linked to
 RT chloroquine-resistant P. falciparum in Southeast Asia and Africa."
 RL Cell 91:593-603(1997).
 DR EMBL: AF030690; AAC47851.1; --
 DR FIK; T09076; T09076.
 DR InterPro: IPR009011; Man_6_P_R_bind.
 SQ SEQUENCE 950 AA; 110601 MW; ED19FEA3B517A378 CRC64;

Query Match 2.8%; Score 8; DB 5; Length 950;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140
 DB 361 SNTLSSPN 368

RESULT 9

ID Q8IBZ8 PRELIMINARY; PRT; 1248 AA.
 AC Q8IBZ8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cg1 protein.
 GN PF07_0035.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
 RA Quail M., Barrell B.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL844506; CAD50843.1; --
 SQ SEQUENCE 1248 AA; 146629 MW; FDBE0EBF1DF769C2 CRC64;

Query Match 2.8%; Score 8; DB 5; Length 1248;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140
 DB 670 SNTLSSPN 677

RESULT 10

Q95NV2 PRELIMINARY; PRT; 39 AA.
 AC Q95NV2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE GM03003p (GM01206p).
 GN BCDNA:GM01206 OR BCDNA:GM03003.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1] _SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY060851; AAL28399.1; --
 DR EMBL: AY060825; AAL28373.1; --
 DR FlyBase; FBgn0047295; BCDNA:GM01206.
 SQ SEQUENCE 39 AA; 4446 MW; 432F8F340E895DC6 CRC64;

Query Match 2.5%; Score 7; DB 5; Length 39;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TVLLQSL 29
 DB 25 TVLLQSL 31

RESULT 11

Q7URQ9 PRELIMINARY; PRT; 73 AA.
 AC Q7URQ9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN RB5505.
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 RT strain 1."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL: BX294142; CAD74279.1; --
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 73 AA; 8265 MW; EF2C586B58E7443F CRC64;

Query Match 2.5%; Score 7; DB 16; Length 73;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 MKSARNS 229

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Db          |||||
1 MKSARNS 7

RESULT 12
Q8KH11      PRELIMINARY;      PRT;      88 AA.
AC Q8KH11;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Conserved hypothetical membrane protein.
GN PB7095.
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1430;
RN [1]
RP SEQUENCE FROM N.A.
RA Berry C., O'Neil S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A.,
RA Harris D., Zaritsky A., Parkhill J.;
RA "The complete sequence and organisation of pBtoxis, the toxin-coding
RT plasmid of Bacillus thuringiensis subsp. israelensis.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF731825; CAD30135.1; -.
KW Hypothetical protein.
SQ SEQUENCE 88 AA; 10480 MW; 545BF036F697398 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLRQLVR 89
Db 19 QLRQLVR 25

RESULT 13
Q870H0      PRELIMINARY;      PRT;      92 AA.
AC Q870H0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sun4p (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Z., Dietrich F.S.;
RA "YNL066W(SUN4) mRNA.";
RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY245796; AAP04346.1; -.
FT NON TER 92
SQ SEQUENCE 92 AA; 9444 MW; 6AA4C3BE7C157567 CRC64;

Query Match      2.5%; Score 7; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 VAVTVVY 37
Db 47 VAVTVVY 53

RESULT 14
Q9HSN3      PRELIMINARY;      PRT;      93 AA.
AC Q9HSN3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vag0151C.
GN VAG0151C.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Laeky S.R., Baliga N.S., Thorsson V., Shrogha J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,
RA Leithauser B., Kellier K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Beck R.F., Pohlchroder M., Spudis J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE004981; AAG18770.1; -.
PIR; F84175; F84175.
KW Complete proteome.
SQ SEQUENCE 93 AA; 9680 MW; AE96B8359F340B49 CRC64;

Query Match      2.5%; Score 7; DB 17; Length 93;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 257 FVSVTNE 263
Db 13 FVSVTNE 19

RESULT 15
Q8PMD7      PRELIMINARY;      PRT;      94 AA.
AC Q8PMD7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein XAC1492.
GN XAC1492.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92825;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Chapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locall E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Secubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE011781; AAM36362.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 94 AA; 11253 MW; A54AD81C115FBF2B CRC64;

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Query Match 2.5%; Score 7; DB 16; Length 94;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 NDRIFVS 259
 DB 65 NDRIFVS 71
 |||||

RESULT 16
 Q9LV97 PRELIMINARY; PRT; 106 AA.
 AC Q9LV97;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Genomic DNA, chromosome 5, Pl clone:MXK3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones";
 RL DNA Res. 7:31-63(2000).
 DR EMBL; AB019236; BAA97292.1; --
 SQ SEQUENCE 106 AA; 12377 MW; A85ECD52EF507B4C CRC64;

Query Match 2.5%; Score 7; DB 10; Length 106;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 IVITVL 25
 DB 17 IVITVL 23
 |||||

RESULT 17
 Q97Y77 PRELIMINARY; PRT; 107 AA.
 AC Q97Y77;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein SS01462.
 GN SS01462.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332296; PubMed=11427726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Aweez M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moors A., Brauso G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; AE006762; AAK41690.1; --
 DR PIR; C90304; C90304.
 DR InterPro; IPR007272; DUF395.

DR Pfam: PF04143; DUF395; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 107 AA; 12018 MW; 9471937E9819A836 CRC64;

Query Match 2.5%; Score 7; DB 17; Length 107;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 PFGAPLV 280
 DB 46 PFGAPLV 52
 |||||

RESULT 18
 Q332M3 PRELIMINARY; PRT; 112 AA.
 ID Q332M3
 AC Q332M3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Truncated resolvase.
 GN TRUNCATED-RES OR SAVP030.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OG Plasmid VRSAP.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Di Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanchisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003367; BAB47538.1; --
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO; GO:0000150; P:recombinase activity; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR006118; Recombinase.
 DR InterPro; IPR006119; resolvase_N.
 DR Pfam; PF00239; resolvase; 1.
 DR PROSITE; PS00397; RECOMBINASES_1; 1.
 DR PROSITE; PS00398; RECOMBINASES_2; 1.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 112 AA; 12884 MW; 1ABB806BBAEDF522 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 112;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 FTVLLQS 28
 DB 106 FTVLLQS 112
 |||||

RESULT 19
 Q7U9A5 PRELIMINARY; PRT; 121 AA.
 ID Q7U9A5
 AC Q7U9A5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical.
 GN SYN00353.
 OS Synecococcus sp. (strain WH8102).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
 OX NCBI_TaxID=84588;
 RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641;
RA Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,
RA Lamerdin J., Regala W., Allen E.E., McCarran J., Paulsen I.,
RA Dufresne A., Partensky F., Webb E.A., Waterbury J.,
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569689; CAE06868.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 121 AA; 13842 MW; CE9C32B4C63811F5 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 121;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 QRVAAHI 126
Db 76 QRVAAHI 82
|||||

RESULT 20
P72087 PRELIMINARY; PRT; 125 AA.
AC P72087;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE Hemolysin A homolog (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491;
RX MEDLINE=97008141; PubMed=8855317;
RA Tinsley C.R., Nassif X.;
RT "Analysis of the genetic differences between Neisseria meningitidis
RT and Neisseria gonorrhoeae: Two closely related bacteria expressing two
RT different pathogenicities.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:11109-11114(1996).
DR EMBL; U56741; AAC44481.1; -.
FT NON_TER 1
FT NON_TER 125
FT NON_TER 125
SQ SEQUENCE 125 AA; 12834 MW; 92D8F57FD4493496 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129
Db 18 AAHITGT 24
|||||

RESULT 21
Q8MM82 PRELIMINARY; PRT; 134 AA.
AC Q8MM82;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE T02C12.4 protein.
GN T02C12.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner A.E.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

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RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z38112; CAD36484.1; -.
DR EMBL; Z35603; CAD36484.1; JOINED.
DR EMBL; Z35603; CAD36496.1; -.
DR EMBL; Z38112; CAD36496.1; JOINED.
DR WormPep; T02C12.4; CE30825.
SQ SEQUENCE 134 AA; 15340 MW; 1DB9A0AD8814E477 CRC64;

Query Match 2.5%; Score 7; DB 5; Length 134;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 EYGLYSI 242
Db 81 EYGLYSI 87
|||||

RESULT 22
Q9YBC2 PRELIMINARY; PRT; 155 AA.
AC Q9YBC2;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein APE1675.
GN APE1675.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000062; BAA80676.1; -.
DR FIR; G72548; G72548.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 155 AA; 16841 MW; 1AA47C685D52939B CRC64;

Query Match 2.5%; Score 7; DB 17; Length 155;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 TLSSPNS 141
Db 88 TLSSPNS 94
|||||

RESULT 23
Q83TU1 PRELIMINARY; PRT; 157 AA.
AC Q83TU1;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

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DE Hypothetical protein.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Newman, and ISP479C;
RA Steinhuber A., Goerke C., Bayer M.G., Doring G., Wolz C.;
RT "Molecular architecture of the regulatory locus sae of Staphylococcus
RL aureus and its impact on the expression of virulence factors.";
DR EMBL: AJ556794; CAD89109.1; -.
DR EMBL: AJ556795; CAD89113.1; -.
KW Hypothetical protein.
SQ SEQUENCE 157 AA; 17665 MW; AF973D8D95D5963E CRC64;

Query Match          2.5%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ASFFGAF 278
Db 90 ASFFGAF 96
|||||

RESULT 24
ID Q9N8D4 PRELIMINARY; PRT; 172 AA.
AC Q9N8D4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acetyltransferase, possible.
GN TB927.1.4490.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU927;
RA Hall N., Berriman M., Lennard N.J., Harris B.R., Gerrard C.S.,
RA Atkin R.J., Barron A.J., Bart-Delabesse E.N., Bowman S.,
RA Bray-Allen S.P., Bringaud F., Clark L.N., Corton C.H., Cronin A.,
RA Davies R., Doggett J., Fraser A., Gruter E., Hall S., Harper D.A.,
RA Hertz-Fowler C., Kay M.P., Leech V., Mayes R., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Saese J., Sharp S., Showkhen R.,
RA Gull K., Barrell B.G., Melville S.E.;
RT "The sequence and analysis of the highly polymorphic chromosome I of
RT the African trypanosome, Trypanosoma brucei."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL929607; CAB95609.1; -.
DR GO: GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR000182; GCN5acetyl_trans.
DR Pfam: PF00583; Acetyltransf; 1.
KW Transferase.
SQ SEQUENCE 172 AA; 19682 MW; B5DD1A59A77E2AB9 CRC64;

Query Match          2.5%; Score 7; DB 5; Length 172;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 NSKNEKA 146
Db 142 NSKNEKA 148
|||||

RESULT 25
Q8P7K6 PRELIMINARY; PRT; 193 AA.
AC Q8P7K6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein XCC2605.
GN XCC2605.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPBP 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fortighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Teal S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL: AE012372; BAM41877.1; -.
DR InterPro: IPR006839; DUF615.
DR InterPro: IPR001232; Skp1.
DR InterPro: IPR008945; Skp1_Skp2.
DR Pfam: PF04751; DUF615; 1.
DR PIRSF: PIRSF016183; UCP016183; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 193 AA; 22001 MW; F00A357929414027 CRC64;

Query Match          2.5%; Score 7; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QLRQLVR 89
Db 138 QLRQLVR 144
|||||

RESULT 26
Q82JU6 PRELIMINARY; PRT; 204 AA.
AC Q82JU6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LipB; lipote-protein ligase B (EC 6.---).
GN LipB OR NEI488.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL: BX321861; CAD85399.1; -.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0009107; P:lipote biosynthesis; IEA.

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DR GO: GO:0006464; P:protein modification; IEA.

DR InterPro: IPR004143; BPL LipA LipB.

DR InterPro: IPR000544; Lipoate_E.

DR Pfam: PF03099; BPL LipA LipB; 1.

DR ProDom: PD006086; Lipoate_E; 1.

DR TIGRFAMs: TIGR00214; LipB; 1.

DR PROSITE: PS01313; LipB; 1.

DR PROSITE: PS01313; LipB; 1.

KW Ligase; Complete proteome.

SQ SEQUENCE 204 AA; 22764 MW; A83F6EF5F0346E61 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 204;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 QQLVRKM 91

Db 97 QQLVRKM 103

RESULT 27

Q8PIX9 PRELIMINARY; PRT; 216 AA.

AC Q8PIX9

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein XAC2766.

GN XAC2766.

OS Xanthomonas axonopodis (pv. citri).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=92829;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=306 / ATCC 13902 / XV 101;

RE MEDLINE=2202145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reilbach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Teal S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities."

RL Nature 417:459-463(2002).

DR EMEL; AE011917; AM37611.1; --

DR InterPro: IPR006839; DUF615.

DR InterPro: IPR001232; Skp1.

DR InterPro: IPR008945; Skp1_skp2.

DR Pfam: PF04751; DUF615; 1.

DR PIRSF: PIRSF016183; UCP016183; 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 216 AA; 24794 MW; 6369B77E20D25B8A CRC64;

Query Match 2.5%; Score 7; DB 16; Length 216;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLQLVR 89

Db 161 QLQLVR 167

RESULT 28

Q9LTD0

AC Q9LTD0 PRELIMINARY; PRT; 217 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE HR-like lesion-inducing protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RE MEDLINE=20277480; PubMed=10819329;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence

RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC

RT clones.";

RL DNA Res. 7:131-135(2000).

DR EMBL; AB025608; BAA95731.1; --

DR InterPro: IPR008637; HR_lesion.

DR Pfam: PF05514; HR_lesion; 1.

DR PFam: PF05514; HR_lesion; 1.

SQ SEQUENCE 217 AA; 25219 MW; F88CDE1A0BEABC4F CRC64;

Query Match 2.5%; Score 7; DB 10; Length 217;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 SFFGAFL 279

Db 88 SFFGAFL 94

RESULT 29

Q89V44

ID Q89V44 PRELIMINARY; PRT; 220 AA.

AC Q89V44

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Brl214 protein.

GN Brl214.

OS Bradyrhizobium japonicum.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bradyrhizobiaceae; Bradyrhizobium.

OX NCBI_TaxID=375;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=USDA 110;

RE MEDLINE=22484998; PubMed=12597275;

RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,

RA Sasamoto S., Watanabe A., Idegawa K., Iriguchi M., Kawashima K.,

RA Kohara M., Matsumoto M., Shimpou S., Tsuruoka H., Wada T., Yamada M.,

RA Tabata S.;

RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium

RT Bradyrhizobium japonicum USDA110.";

RL DNA Res. 9:189-197(2002).

DR EMBL; AP005939; BAC46479.1; --

DR InterPro: IPR000437; Prok_LipoProt.S.

DR PROSITE: PS00013; PROK_LIPOPROTEIN; 1.

KW Complete proteome.

SQ SEQUENCE 220 AA; 23332 MW; 0AD03221F4C1A350 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 220;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 113 LVREGE 119
Db 110 LVREGE 116

RESULT 30
Q8DFN8 PRELIMINARY; PRT; 222 AA.
AC Q8DFN8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Uncharacterized protein conserved in bacteria.
GN V10168.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=QWCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus QWCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016797; AAC08706.1; -.
KW Complete proteome.
SQ SEQUENCE 222 AA; 24807 MW; 94A0EF9F43F33FAD CRC64;

Query Match 2.5%; Score 7; DB 16; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GIFELKE 252
Db 190 GIFELKE 196

RESULT 31
ID P90611 PRELIMINARY; PRT; 231 AA.
AC P90611;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE H4 gene.
GN H4.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BK;
RX MEDLINE=20542029; PubMed=11087916;
RA Brydges S.D., Sherman G.D., Nockemann S., Loyens A., Daubener W.,
RA Dubremetz J.F., Curruheres V.B.;
RT "Molecular characterization of TgMIC5, a proteolytically processed
RT antigen secreted from the micronemes of Toxoplasma gondii.";
RL Mol. Biochem. Parasitol. 111:51-66(2000).
DR EMBL; Y09782; CAA70921.1; -.
SQ SEQUENCE 231 AA; 25984 MW; 9C5B0E4690B36314 CRC64;

Query Match 2.5%; Score 7; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FQEIKE 198
Db 137 FQEIKE 143

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RESULT 32
Q9EZK4 PRELIMINARY; PRT; 247 AA.
AC Q9EZK4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Rot-like protein Rlp.
GN RLP.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA McNamara P.J., Milligan-Monroe K., Proctor R.A.;
RT "The Isolation and Characterization of rlp, an Activator of the
RT Staphylococcus aureus Virulence Factor Regulator Pathway Encoded by
RT agr.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288788; AAG45334.2; -.
SQ SEQUENCE 247 AA; 29792 MW; D078366866F60B2B CRC64;

Query Match 2.5%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
Db 91 RIFVSVT 97

RESULT 33
Q99RD5 PRELIMINARY; PRT; 247 AA.
AC Q99RD5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SarH2 protein (Staphylococcal accessory regulator A homolog).
GN SARH2 OR SAV2499 OR SA2287 OR MW2418.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP003365; BAB58661.1; -.
DR EMBL; AP003137; BAB43590.1; -.
DR EMBL; AP004830; BAB96283.1; -.
DR PIR; D90053; D90053.

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KW Complete proteome.
SQ SEQUENCE 247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;

Query Match      2.5%; Score 7; DB 16; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 RIFVSVT 261
Db 91 RIFVSVT 97

RESULT 34
O94262 PRELIMINARY; PRT; 251 AA.
AC O94262;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN SPBP8B7.13.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-.
RA Beck A., Reinhardt R., Lyne M., Rajandream M.A., Barrell B.G.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL032684; CAA1798.1; -.
DR PIR; T40807; T40807.
DR GeneDB SPombe; SPBP8B7.13; -.
KW Hypothetical protein.
SQ SEQUENCE 251 AA; 27746 MW; C631E344FDC0D686 CRC64;

Query Match      2.5%; Score 7; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 DPNDDES 72
Db 73 DPNDDES 79

RESULT 35
O98D64 PRELIMINARY; PRT; 253 AA.
AC O98D64;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein ml14839.
GN Ml14839.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003005; BAB51407.1; -.
DR InterPro; IPR00160; GODEF.

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DR Pfam; PF00990; GODEF; 1.
DR SMART; SM00267; DUF1; 1.
DR TIGRFAMs; TIGR00254; GODEF; 1.
DR PROSITE; PS00887; GODEF; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 253 AA; 27656 MW; 358A4F06B9B66C8E CRC64;

Query Match      2.5%; Score 7; DB 16; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 FGAFVVG 281
Db 168 FGAFVVG 174

RESULT 36
O81W00 PRELIMINARY; PRT; 271 AA.
AC O81W00;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hydrolase, alpha/beta fold family.
GN BA3877.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
DR EMBL; AE017036; AAP27611.1; -.
DR TIGR; BA3877; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR00073; A/b hydrolase.
DR InterPro; IPR003089; AB Hydrolase.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00561; abhydrolase_1.
DR PRINTS; PR00111; ABHYDROLASE.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 271 AA; 31338 MW; D01E8F4D025FF187 CRC64;

Query Match      2.5%; Score 7; DB 16; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 RFQEEIK 197
Db 170 RFQEEIK 176

RESULT 37
O8R0L0 PRELIMINARY; PRT; 293 AA.
ID O8R0L0
AC O8R0L0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026645; AAH26645.1; --
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 293 AA; 33723 MW; 642B913C78884195 CRC64;

Query Match 2.5%; Score 7; DB 11; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 LRTSEET 99
DB 5 LRTSEET 11

RESULT 38
Q823E7 PRELIMINARY; PRT; 296 AA.
AC Q823E7;
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J., Holtzapfel E., Khouri H., Federova N.B., Carty H.A.,
RA Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
RA Fraser C.M.;
RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaeae."
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AE016995; AAP05216.1; --
DR TIGR; CCA00471; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009249; P:protein-lipoylation; IEA.
DR InterPro; IPR001640; LGT.
DR Pfam; PF01790; LGT; 1.
DR ProDom; PD005412; LGT; 1.
DR TIGRPFAM; TIGR00544; lgt; 1.
KW Lipoprotein; transferase; Complete proteome.
SQ SEQUENCE 296 AA; 33457 MW; 1E148CA397939B64 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GIACFLK 59
DB 278 GIACFLK 284

RESULT 39
Q8E3I3 PRELIMINARY; PRT; 298 AA.
ID Q8E3I3
AC Q8DXW4 PRELIMINARY; PRT; 298 AA.
Q8DXW4
AC Q8DXW4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Membrane protein, putative.
GN SAG1731.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=12200547;
RA Tettelin H., Massignani V., Cielesiewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Federova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014270; AAN00594.1; --
DR TIGR; SAG1731; --
KW Complete proteome.
SQ SEQUENCE 298 AA; 32410 MW; 5BF7720198133368 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 VLLQSLC 30
DB 92 VLLQSLC 98

RESULT 40
Q8DXW4 PRELIMINARY; PRT; 298 AA.
ID Q8DXW4
AC Q8DXW4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Membrane protein, putative.
GN SAG1731.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=12200547;
RA Tettelin H., Massignani V., Cielesiewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Federova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014270; AAN00594.1; --
DR TIGR; SAG1731; --
KW Complete proteome.
SQ SEQUENCE 298 AA; 32410 MW; 5BF7720198133368 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 VLLQSLC 30

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Db          92 VLLQSLC 98
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RESULT 41
Q96QL7      PRELIMINARY;      PRT;      318 AA.
AC Q96QL7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to cAMP responsive element binding protein-like 1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strauberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008394; AAB08394.1; -.
DR EMBL; BT007042; AAP35691.1; -.
SQ SEQUENCE 318 AA; 33894 MW; D70E20D5409C165B CRC64;

Query Match          2.5%; Score 7; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          23 TVLIQSL 29
|||||
Db          266 TVLIQSL 272
|||||

RESULT 42
Q9VI33      PRELIMINARY;      PRT;      322 AA.
AC Q9VI33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG2336 protein (AT02555p).
GN CG2336
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Makos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Rosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kaulush F., Karpen G.H., Ke Z., Kennison J.A., Kibegwa C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Neilson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Scapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarini H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuncio J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003674; AAF54111.1; -.
DR EMBL; AB009235; AAL89973.1; -.
DR FlyBase; FBgn0037455; CG2336.
SQ SEQUENCE 322 AA; 36891 MW; D8680A7A63BB5988 CRC64;

Query Match          2.5%; Score 7; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          207 VQIYKY 213
|||||
Db          16 VQIYKY 22
|||||

RESULT 43
Q9PEN6      PRELIMINARY;      PRT;      327 AA.
AC Q9PEN6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein XF0992.
GN XF0992.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.R., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.B., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,

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RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Heheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.B. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.P., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjowski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
RT "The genome sequence of the plant pathogen Xylella fastidiosa";
RL Nature 406:151-159(2000).
DR EMBL; AB003937; AAF83802.1; --
DR PIR; H82736; H82736.
DR GO; GO:0003824; F.catalytic activity; IEA.
DR InterPro; IPR000379; Ser_estr.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 327 AA; 35553 MW; 96A5841EB1A08E90 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 111 SPLVR 117
Db 164 SPLVR 170

RESULT 44
Q9ZKY9 PRELIMINARY; PRT; 329 AA.
AC Q9ZKY9
DT 01-MAY-1999 (TREMELrel. 10, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ADP-L-glycero-D-MANNOHEPTOSE-6-epimerase.
GN GMHD OR JHP0793.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori";
RL Nature 397:176-180(1999).
DR EMBL; AB001509; AAD06369.1; --
DR PIR; D71887; D71887.
DR GO; GO:0003824; F.catalytic activity; IEA.
DR GO; GO:0009225; P.nucleotide-sugar metabolism; IEA.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
KW Complete proteome.
SQ SEQUENCE 329 AA; 37351 MW; DD1003F6A8C7A720 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RSNTISS 138
Db 46 RSNTISS 52

RESULT 45
Q7VJZ3 PRELIMINARY; PRT; 343 AA.
ID Q7VJZ3
AC Q7VJZ3
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE DTPD-D-glucose 4,6-dehydratase (EC 4.2.1.46).
GN HH0099.
OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=32025;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 51449 / 3B1;
RX MEDLINE=22709201; PubMed=12810954;
RA Suarbaum S., Josenhans C., Sterzenbach T., Dreescher B., Brandt P.,
RA Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
RT "The complete genome sequence of the carcinogenic bacterium
RT Helicobacter hepaticus";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
DR EMBL; AE017144; AAP76696.1; --
KW Lyase; Complete proteome.
SQ SEQUENCE 343 AA; 38920 MW; B528F6F2710A40D2 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 343;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 YIYKTS 215
Db 329 YIYKTS 335

RESULT 46
O84846 PRELIMINARY; PRT; 354 AA.
ID O84846
AC O84846;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Hypothetical protein CT839.
GN CT839.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=D/OW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis";
RL Science 282:754-759(1998).
DR EMBL; AE001356; AAC68436.1; --
DR PIR; G71465; G71465.
DR GO; GO:0016021; C.integral to membrane; IEA.
DR InterPro; IPR005495; YjgP_YjgQ.
DR Pfam; PF03739; YjgP_YjgQ; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 354 AA; 40065 MW; AD79C8F2CD59F4E5 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 354;

```
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
Db 150 KENDRIF 156

RESULT 47
Q9PL80 PRELIMINARY; PRT; 354 AA.
AC Q9PL80
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Hypothetical protein TC0227.
GN TC0227
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Ni99;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
  White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S.,
  Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
  Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
  Eisen J., Fraser C.M.;
RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
  pneumoniae AR39.";
RT Nucleic Acids Res. 28:1397-1406(2000).
RL EMBL; AF002289; AAF39099.1; --
DR PIR; A81728; A81728.
DR TIGR; TC0227; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR005495; YjgP_YjgP.
DR Pfam; PF03739; YjgP_YjgP.1.
DR KQ Hypothetical protein; Complete proteome.
SQ SEQUENCE 354 AA; 40145 MW; E6A1317A124C10D1 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
Db 150 KENDRIF 156

RESULT 48
Q9AVE6 PRELIMINARY; PRT; 359 AA.
AC Q9AVE6
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE OSTATC protein.
GN OSTATC OR B1080D07.14.
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RX MEDLINE=21140310; PubMed=11244106;
RA Agrawal G.K., Yamazaki M., Kobayashi M., Hirochika R., Miyao A.,
  Hirochika H.;
RT "Screening of the Rice Viviparous Mutants Generated by Endogenous
  Retrotransposon Tos17 Insertion. Tagging of a Zeaxanthin Epoxidase
  Gene and a Novel OSTATC Gene.";

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
Db 150 KENDRIF 156

RESULT 49
Q98SU0 PRELIMINARY; PRT; 361 AA.
AC Q98SU0
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE K-Cl cotransporter (Fragment).
GN KCC.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
  Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Mount D.B., Gamba G.;
RT "Partial sequence of xKCC, a K-Cl cotransporter from Xenopus laevis.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF325505; AAK28520.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR000622; KCL_cotranspt1.
DR Pfam; PF03522; KCL_Cotrans_1; 1.
FT NON TER 1
SQ SEQUENCE 361 AA; 41551 MW; 129A632D1D2EDB64 CRC64;

Query Match 2.5%; Score 7; DB 13; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 LVRERGP 119
Db 347 LVRERGP 353

RESULT 50
Q8WPJ2 PRELIMINARY; PRT; 367 AA.
AC Q8WPJ2
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Endo-1,4-mannanase precursor (EC 3.2.1.78).
OS Mytilus edulis (Blue mussel).
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OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gill;
RA Xu B., Janson J.C., Sellos B.;
RT "An endo-1,4-beta-D-mannanase gene isolated from mytilus edulis.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271365; CAC81056.1; -.
DR GO; GO:0016798; F-hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0016985; F-mannan endo-1,4-beta-mannosidase activity; IEA.
DR GO; GO:0005975; P-carbohydrate metabolism; IEA.
KW Signal; Hydrolase; Glycosidase.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 367 ENDO-1,4-MANNANASE.
SQ SEQUENCE 367 AA; 40956 MW; B36AE03418D2EA86 CRC64;

Query Match 2.5%; Score 7; DB 5; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 KNEKALG 148
DB 164 KNEKALG 170

RESULT 51
Q7U3W6 PRELIMINARY; PRT; 374 AA.
ID Q7U3W6
AC Q7U3W6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Peptide chain release factor RF-2.
GN PRFB OR SYNW2311.
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641;
RA Palenik B., Bransham B., Larimer F.W., Land M., Hauser L., Chain P.,
RA Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
RA Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569695; CA808826.1; -.
KW Complete proteome.
SQ SEQUENCE 374 AA; 41775 MW; A1FC8CE06FBB444 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 LRTSEET 99
DB 336 LRTSEET 342

RESULT 52
Q9L5E1 PRELIMINARY; PRT; 375 AA.
ID Q9L5E1
AC Q9L5E1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Orf, hypothetical protein (Hypothetical protein).
GN R0207 OR HCM1.114.
OS Salmonella typhi.
OX Plasmid R27, and Plasmid pHCM1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.

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OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=R27;
RX MEDLINE=20280091; PubMed=10773089;
RA Sherburne C.K., Lawley T.D., Gilmour M.W., Blattner F.R., Burland V.,
RA Grotbeck E., Rose D.J., Taylor D.E.;
RT "The complete DNA sequence and analysis of R27, a large IncHI plasmid
from Salmonella typhi that is temperature sensitive for transfer.";
EL Nucleic Acids Res. 28:2177-2186(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CT18; PLASMID=pHCM1;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Holden M.T.G., Sebaihia M.,
RA Churcher C., Mungall K.L., Bentley S.D., Chillingworth T., Conerton P.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Farrar J.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar typhi C18.";
RL Nature 413:848-852(2001).
DR EMBL; AF250878; AAF70043.1; -.
DR EMBL; AL513383; CAD09712.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 375 AA; 42554 MW; 98669A1E335525C0 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 LKQMDK 48
DB 224 LKQMDK 230

RESULT 53
Q8TWS8 PRELIMINARY; PRT; 375 AA.
ID Q8TWS8
AC Q8TWS8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Uncharacterized conserved protein.
GN MK0954.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL; AE010385; AAM02167.1; -.
DR InterPro; IPR008934; AcPase VanPerase.
DR InterPro; IPR002803; DUF100.
DR Pfam; PF01950; DUF100; 1.
DR ProDom; PD014260; DUF100; 1.
KW Complete proteome.
SQ SEQUENCE 375 AA; 41620 MW; 3A9F8E7BB626464C CRC64;

Query Match 2.5%; Score 7; DB 17; Length 375;

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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LRNGELV 175
Db 307 LRNGELV 313

RESULT 54
Q99SW4 PRELIMINARY; PRT; 379 AA.
AC Q99SW4;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DE BLR2286 protein.
GN BLR2286.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=2248498; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005943; BAC47551.1; -.
KW Complete proteome.
SQ SEQUENCE 379 AA; 40061 MW; 30D67BCB25880B61 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 GQQRVA 124
Db 170 GQQRVA 176

RESULT 55
Q9LTH1 PRELIMINARY; PRT; 389 AA.
AC Q9LTH1;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 4-nitrophenylphosphatase-like.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025605; BAA98057.1; -.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR006357; HAD_SF_IIA.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
DR TIGRFAMs; TIGR01460; HAD-SF-IIA; 1.

DR TIGRFAMs; TIGR01452; PGP euk; 1.
SQ SEQUENCE 389 AA; 43131 MW; 96E3D9A7BC4E0583 CRC64;

Query Match 2.5%; Score 7; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 VLLQSLC 30
Db 345 VLLQSLC 351

RESULT 56
Q9PCZ3 PRELIMINARY; PRT; 401 AA.
AC Q9PCZ3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE Hypothetical protein XF1611.
GN XF1611.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Faccinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Frega J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohlseil J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.D., Martins E.M.F., Matekuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa."
RL Nature 406:151-159(2000).
DR EMBL; AE003988; AAF84420.1; -.
DR PIR; C82660; C82660.
DR InterPro; IPR008928; Glyco trans fhp.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 401 AA; 46935 MW; B773581D85270510 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 DAEGYGLY 240
Db 157 DAEGYGLY 163

RESULT 57

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Q87CC1
ID Q87CC1 PRELIMINARY; PRT; 401 AA.
AC Q87CC1;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Conserved hypothetical protein.
GN PD1162.
OS Xyllella fastidiosa (strain Temeculal / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xyllella.
OX NCBI_TaxID=1831190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22421331; PubMed=12533478;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H.,
RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
RA Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
RA Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA Leon S.G., Oliveira A.R., Rosa V.B. Jr., Sassaki F.T., Sena J.A.D.,
RA de Souza A.A., Truffi D., Teukumo F., Yanai G.M., Zaros L.G.,
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitajima J.P.;
RT "Comparative analyses of the complete genome sequences of Pierce's
RT disease and citrus variegated chlorosis strains of Xylella
RT fastidiosa."
RL J. Bacteriol. 185:1018-1026(2003).
RL DR EMBL; AB012557; AAO29015.1; -.
RL InterPro: IPR008928; Glyco trans 6hp.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 401 AA; 46925 MW; 2380EA4DB84D2944 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 DAEYGLY 240
DB 157 DAEYGLY 163
|||||

RESULT 58
Q9H766 PRELIMINARY; PRT; 402 AA.
AC Q9H766;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein FLJ21240.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Colon;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Oiyashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isoigai T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK024893; BAB15032.1; -.
DR Genbank; HGNC:23000; TMC7.
KW Hypothetical protein.
SQ SEQUENCE 402 AA; 46254 MW; 716C111B5B794DC4 CRC64;

Query Match 2.5%; Score 7; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 YKSGIA 55
|||||

RESULT 59
Q9UX27 PRELIMINARY; PRT; 404 AA.
AC Q9UX27;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Amidophosphoribosyltransferase (ATASE) (Glutamine
DE phosphoribosylpyrophosphate amidotransferase) (GPAT) (PUPF-2)
DE (EC 2.4.2.14).
GN PUPF-2 OR SS00633 OR C08_016.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=20165948; PubMed=10701121;
RA Charlebois R.L., Singh R.K., Curtis B., Duguet M., Erauso G., Chow C.,
RA Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D.,
RA Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,
RA Kuswaha N., Lafleur E., Medina N., Peng X., Penny S.D., She Q.,
RA St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F.,
RA Ragan M.A., Sensen C.W.;
RT "Gene content and organization of a 281-kbp contig from the genome of
RT the extremely thermophilic archaeon, Sulfolobus solfataricus P2."
RL Genome 43:116-136(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=1142726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA De Moers A., Erauso G., Fletcher C., Gordon P.M.K., Curtis B.A.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; Y18930; CAB57667.1; -.
DR EMBL; AE006691; AAK40942.1; -.
DR PIR; G90210; G90210.
DR HSSP; P00497; 1GPH.
DR GO; GO:0004044; F:amidophosphoribosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0009116; P:nucleoside metabolism; IEA.
DR InterPro; IPR000583; GATase 2.
DR InterPro; IPR002375; PTPase trans.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00310; GATase 2; 1.
DR Pfam; PF00156; Pribosytiran; 1.
DR PROSITE; PS00103; PUR PYR PR TRANSFER; 1.
KW Glycosyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 404 AA; 44839 MW; DFFFD11A07FD8A0 CRC64;

Query Match 2.5%; Score 7; DB 17; Length 404;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 RTSBETI 100
|||||
DB 29 RTSBETI 35
|||||

us-10-662-429-2.0ligo.rspt
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db 35 YKSGIA 41

RESULT 60

Q99XN8 PRELIMINARY; PRT; 406 AA.
AC Q99XN8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative integral membrane protein.
GN LMP OR SPY2120.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006631; AAK34765.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00083; sugar tr; 1.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
KW Complete proteome.
SQ SEQUENCE 406 AA; 45344 MW; 16AF61AF1E540F7E CRC64;

Query Match 2.5%; Score 7; DB 16; Length 406;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QLQLVR 89

| | | | |

Db 12 QLQLVR 18

RESULT 61

Q9NZ26 PRELIMINARY; PRT; 406 AA.
AC Q9NZ26;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative integral membrane protein.
GN SPM18_2178.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).

DR EMBL; AE010119; AAL98622.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00083; sugar tr; 1.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 406 AA; 45475 MW; CC36336DDB9FF8D4 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 406;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QLQLVR 89

| | | | |

Db 12 QLQLVR 18

RESULT 62

Q8K5J7 PRELIMINARY; PRT; 406 AA.
AC Q8K5J7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative integral membrane protein.
GN LMP OR SPY1804 OR SPS1802.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mamarelli N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE014171; AAM80411.1; -
DR EMBL; AP005146; BAC64897.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00083; sugar tr; 1.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 406 AA; 45499 MW; 0824D1758512AF2B CRC64;

Query Match 2.5%; Score 7; DB 16; Length 406;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      83 QLRQLVR 89
DB      12 QURQLVR 18

RESULT 63
Q8S179
ID Q8S179 PRELIMINARY; PRT; 414 AA.
AC Q8S179;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 25, Last annotation update)
DE Putative RNA polymerase III subunit.
GN B1144G04.24.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
   clone:B1144G04."
RL EMBL; AF003335; BAB90033.1; -.
DR Gramine; Q8S179; -.
DR InterPro; IPR008806; RNA_pol_Rpc82.
DR Pfam; PF05645; RNA_pol_Rpc82; 1.
SQ SEQUENCE 414 AA; 47142 MW; EB95244618E143DD CRC64;

Query Match      2.5%; Score 7; DB 10; Length 414;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      113 LVRERGP 119
DB      322 LVRERGP 328

RESULT 64
Q8KIU0
ID Q8KIU0 PRELIMINARY; PRT; 417 AA.
AC Q8KIU0;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Similar to glycosyl transferases group 1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22053227; PubMed=12057956;
RA Raymond C.K., Sims E.H., Kas A., Spencer D.H., Kutayavin T.V.,
   Ivey R.G., Zhou Y., Kaul R., Clendenning J.B., Olson M.V.;
RT "Genetic Variation at the O-Antigen Biosynthetic Locus in Pseudomonas
   aeruginosa."
RL J. Bacteriol. 184:3614-3622(2002).
DR EMBL; AF498403; AAM27604.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biogenesis; IEA.
DR InterPro; IPR001296; Glyco_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Transferase.
SQ SEQUENCE 417 AA; 46576 MW; 2B3E3EF2B57FE76E CRC64;

Query Match      2.5%; Score 7; DB 2; Length 417;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      272 ASFFGAF 278
DB      95 ASFFGAF 101

RESULT 65
Q8KI00
ID Q8KI00 PRELIMINARY; PRT; 417 AA.
AC Q8KI00;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Similar to glycosyl transferases group 1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22053227; PubMed=12057956;
RA Raymond C.K., Sims E.H., Kas A., Spencer D.H., Kutayavin T.V.,
   Ivey R.G., Zhou Y., Kaul R., Clendenning J.B., Olson M.V.;
RT "Genetic Variation at the O-Antigen Biosynthetic Locus in Pseudomonas
   aeruginosa."
RL J. Bacteriol. 184:3614-3622(2002).
DR EMBL; AF498415; AAM27788.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biogenesis; IEA.
DR InterPro; IPR001296; Glyco_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Transferase.
SQ SEQUENCE 417 AA; 46410 MW; 2265075495ABCE78 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 417;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      272 ASFFGAF 278
DB      95 ASFFGAF 101

RESULT 66
Q8I514
ID Q8I514 PRELIMINARY; PRT; 420 AA.
AC Q8I514;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
   Carlton J.M., Pain N., Nelson K.E., Bowman S., Paulsen I.T., James K.,
   Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
   Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
   Pertea M., Allen J., Haft D., Mather M.W., Vaidya A.B.,
   Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
   McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
   Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
   Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
   falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AE014851; RAN36483.1; -.
KW Hypothetical protein.

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Db      171 LGRKINS 177

RESULT 70
ID O83835 PRELIMINARY; PRT; 427 AA.
AC O83835;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nitrogen fixation protein (NIFS-2).
GN TP0863.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artach P., Bowman C., Cotton W.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL Science 281:375-388(1998).
DR EMBL; AE001256; AAC65826.1; -.
DR FIr; G71272; G71272.
DR TIGR; TP0863; -.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000192; Aminotrans_V.
DR Pfam; PF00266; aminotran_5; 1.
DR Complete proteome.
SQ SEQUENCE 427 AA; 45732 MW; 0B5247CDBFA901AD CRC64;

Query Match 2.5%; Score 7; DB 16; Length 427;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TGTGRGS 133
Db 166 TGTGRGS 172

RESULT 71
QHSA2 PRELIMINARY; PRT; 428 AA.
ID Q9HSA2
AC Q9HSA2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Zinc metalloproteinase homolog.
GN CAAX OR VNG03296.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsen V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1."

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RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE004992; AAG18905.1; -.
DR PIR; E84192; E84192.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001915; Peptidase_M48.
DR Pfam; PF01435; Peptidase_M48; 1.
DR Complete proteome.
SQ SEQUENCE 428 AA; 45621 MW; 8E421F4FF1C1542D CRC64;

Query Match 2.5%; Score 7; DB 17; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 SSRSGHS 162
Db 237 SSRSGHS 243

RESULT 72
Q9Z913 PRELIMINARY; PRT; 429 AA.
ID Q9Z913
AC Q9Z913;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE GMP synthase.
GN GUAA OR CPN0171 OR CP0599 OR CPB0173.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalkan S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."
RT Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=JL38;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA."
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RX Geng M.M., Schumacher A., Muehlendorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marte R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT other Chlamydia strains based on whole genome sequence analysis."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE001604; AAF18324.1; -.
DR EMBL; AE002218; AAF38415.1; -.
DR EMBL; AP002545; BAA98381.1; -.
DR EMBL; AE017157; AAP98106.1; -.

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DR PIR: B72109; B72109.
DR PIR: C86512; C86512.
DR HSPF: P04079; 1GPM.
DR TIGR: CP0599; -.
DR GO: GO:000524; F:ATP binding; IEA.
DR GO: GO:0003824; F:catalytic activity; IEA.
DR GO: GO:0003922; F:GMP synthase (glutamine-hydrolyzing) activity; IEA.
DR GO: GO:0006177; P:GMP biosynthesis; IEA.
DR GO: GO:0006164; P:purine nucleotide biosynthesis; IEA.
DR InterPro: IPR006220; Anth_synthII.
DR InterPro: IPR000991; GATase 1.
DR InterPro: IPR001674; GMP synth C.
DR InterPro: IPR004739; GMP synth_N.
DR Pfam: PF00117; GATase; 1.
DR Pfam: PF00958; GMP synth C; 1.
DR PRINTS: PR00097; ANTSNTHASEII.
DR PRINTS: PR00096; GATASE.
DR TIGRFAMs: TIGR00888; guaA_Nterm; 1.
KW Complete proteome.
SQ SEQUENCE 429 AA; 48242 MW; DBFD3C681109BFEC CRC64;

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Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 ESSRSGH 161
Db 248 ESSRSGH 254
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RESULT 73
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AC Q80ZJ8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC048916; AAH48916.1; -.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; efhnd; 2.
DR SMART; SM00054; EFh; 2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 435 AA; 49006 MW; BA711CSA7DB7EB8A CRC64;

Query Match 2.5%; Score 7; DB 11; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 LRTSET 99
Db 147 LRTSET 153
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RESULT 74
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AC Q8SWZ1; Q9V5Q6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RH55021p (CG12344-PA).

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GN CG12344.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbavani A., Carlson J.,
RA Campe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Puri V., Resee M.G.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.B., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush C., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang Z.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster."
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,
RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
RA Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J.,
RA Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F.,
RA Whitfield B.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,
RA Lewis S.E.;
RL "Annotation of Drosophila melanogaster genome."
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

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[5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AY094938; AAM11291.1; -.
DR EMBL; AE003828; AAF58743.3; -.
DR FlyBase; FBgn0033558; CG12344.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005230; F: extracellular ligand-gated ion channel acti. . .; IEA.
DR GO; GO:0005216; F: ion channel activity; IEA.
DR GO; GO:0030594; F: neurotransmitter receptor activity; IEA.
DR GO; GO:0006811; P: ion transport; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_Channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 449 AA; 51256 MW; 79EE29E409FDC648 CRC64;

Query Match 2.5%; Score 7; DB 5; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 PILLMKS 225
Db 442 PILLMKS 448
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AC Q7WQF5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sensor kinase protein.
GN BB0378.
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=RB50 / ATCC BAA-588;
RC MEDLINE=22827954; PubMed=12910271;
RX Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cardano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640438; CAE30876.1; -.
KW Kinase; Complete proteome.
SQ SEQUENCE 457 AA; 50053 MW; 21C76EBD1CB46265 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 457;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 LLMKSR 227
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Db 233 LLMKSR 239
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Search completed: March 23, 2004, 09:23:42
Job time : 51 secs

Tue Mar 23 11:15:49 2004

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:12:39 ; Search time 23 seconds
(without alignments)
545.440 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNLKQMDKXKSGIACFL.....NEHLMDHEASFFGAFLVG 243

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 317993

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/2/iaa/6D COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	72.3	177	3	US-09-105-343A-7
2	850	66.0	161	4	US-09-565-423-7
3	654	50.8	183	3	US-09-105-343A-8
4	446	34.7	85	4	US-09-632-287A-12
5	291	22.6	101	1	US-08-670-354-4
6	291	22.6	101	3	US-09-320-424-4
7	291	22.6	101	4	US-09-825-563-4
8	291	22.6	101	5	US-09-10895-4
9	245.5	19.1	87	4	US-09-632-287A-13
10	228.5	17.8	173	4	US-09-396-937-10
11	228.5	17.8	173	4	US-09-396-937-12
12	228.5	17.8	182	4	US-09-396-937-8
13	210	16.3	187	4	US-09-396-937-16
14	208	16.2	188	4	US-09-396-937-14
15	202.5	15.7	173	4	US-09-396-937-20
16	195.5	15.2	173	4	US-09-396-937-18
17	189.5	14.7	173	4	US-08-339-214-22
18	182	14.1	138	4	US-08-339-214-20
19	181.5	14.1	178	4	US-08-339-214-84
20	181.5	14.1	179	3	US-08-649-100-9
21	181.5	14.1	179	3	US-08-339-214-6
22	179	13.9	137	4	US-08-339-214-18
23	178	13.8	145	3	US-08-330-172-5
24	178	13.8	145	3	US-09-375-419-5
25	177.5	13.6	179	4	US-08-339-214-14
26	175.5	13.6	179	4	US-08-584-031-17
27	175	13.6	152	4	US-09-496-118B-8

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Sequence 80, Appl
Sequence 4, Appl
Sequence 22, Appl
Sequence 79, Appl
Sequence 83, Appl
Sequence 8, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 82, Appl
Sequence 1, Appl
Sequence 4, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 39, Appl

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240 4 US-09-072-993C-4
240 4 US-09-653-285-1
174 4 US-09-131-237C-2
208 4 US-09-027-287-39

ALIGNMENTS

RESULT 1
US-09-105-343A-7
; Sequence 7, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; FOR TREATMENT AND DIAGNOSIS OF DISEASE
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-7

Query Match 72.3%; Score 930; DB 3; Length 177;
Best Local Similarity 99.4%; Pred. No. 1.2e-88;
Matches 176; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY

67 EKQNIPLVRGPQVAAHITGRTGRSNTLSPNSKNEKALGRKINSWESSRSHSFL 126

Db 1 EQQNIPLVRERQORVAHITGRGNTLSSPNSKNEKALGRKINSWESSRSHSFL 60
QY 127 SNLHRLNGELVHKGFYIYSQYFRQOEIKENTKNDKQMVQYIYKYSYDPDILMK 186
Db 61 SNLHRLNGELVHKGFYIYSQYFRQOEIKENTKNDKQMVQYIYKYSYDPDILMK 120
QY 187 SARNSCWSKDAEYGLYSTYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFV 243
Db 121 SARNSCWSKDAEYGLYSTYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFV 177

RESULT 2

US-09-565-423-7
; Sequence 7, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565.423
; CURRENT FILING DATE: 2000-05-05
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-7

Query Match 66.0%; Score 850; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.1e-80;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSHSFLSNLHRLNGELVHK 142
Db 1 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSHSFLSNLHRLNGELVHK 60
QY 143 FYIYSQYFRQOEIKENTKNDKQMVQYIYKYSYDPDILMKSNRNSCWSKDAEYGLV 202
Db 61 FYIYSQYFRQOEIKENTKNDKQMVQYIYKYSYDPDILMKSNRNSCWSKDAEYGLV 120
QY 203 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFV 243
Db 121 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFV 161

RESULT 3

US-09-105-343A-8
; Sequence 8, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; FILE REFERENCE: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US98/02859
; APPLICATION NUMBER: 12-FEB-1998
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048, US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:

; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-8

Query Match 50.8%; Score 654; DB 3; Length 183;
Best Local Similarity 68.7%; Pred. No. 5.6e-60;
Matches 125; Conservative 22; Mismatches 29; Indels 6; Gaps 1;

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QY 127 SNLHRLNGELVHKGFYIYSQYFRQOEIKENTKNDKQMVQYIYKYSYDP 180
Db 61 SNLHRLNGELVHKGFYIYSQYFRQOEIKENTKNDKQMVQYIYKYSYDP 120
QY 181 PIVLMKSARNCSWSDAEYGLYSTYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAF 240
Db 121 PIVLMKSARNCSWSDAEYGLYSTYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAF 180
QY 241 LV 242
Db 181 II 182

RESULT 4

US-09-632-287A-12
; Sequence 12, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Pbm, A No. 6521422el Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-632-287A-12

Query Match 34.7%; Score 446; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 7.1e-39;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 ERGQORVAHITGRGNTLSSPNSKNEKALGRKINSWESSRSHSFLSNLHRLNGELV 137

GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 597-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-4

Query Match 22.6%; Score 291; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGTACTLKEDDSYWDNDDESMNSPCQVKWQLRQLVRK 52
DB 39 TNELKQMDKYSKSGIACELKEDDSYWDNDDESMNSPCQVKWQLRQLVRK 90

RESULT 9
US-09-632-287A-13
Sequence 13, Application US/09632287A
Patent No. 6521422
GENERAL INFORMATION:
APPLICANT: Hsu, Hailing
APPLICANT: Wooden, Scott K
APPLICANT: Boyle, William J
TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
FILE REFERENCE: 01017/35550A
CURRENT APPLICATION NUMBER: US/09/632,287A
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/147,294
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 87
TYPE: PRT
ORGANISM: Mouse

US-09-632-287A-13

Query Match 19.1%; Score 245.5; DB 4; Length 87;
Best Local Similarity 65.8%; Pred. No. 4.7e-18;
Matches 50; Conservative 9; Mismatches 14; Indels 3; Gaps 1;
QY 81 PORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHIE 140
DB 4 POKVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHIE 63
QY 141 KGFYIYSOTYRFR 156
DB 64 E----YIYSOTYRFRQE 76

RESULT 10

US-09-396-937-10
Sequence 10, Application US/09396937
Patent No. 6645500
GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
FILE REFERENCE: 22021 PC 1
CURRENT APPLICATION NUMBER: US/09/396,937
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 173
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA encoding
OTHER INFORMATION: murine OPG, residues 158-316, fused to His tag
US-09-396-937-10

Query Match 17.8%; Score 228.5; DB 4; Length 173;
Best Local Similarity 34.2%; Pred. No. 7.4e-16;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

QY 86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHIEKGY 145
DB 22 AHLT-----INAAISPGSHKVTL-----SSWYHDR-GWAKISNTLSNGKLRVNDGFFY 71
QY 146 IYSQTYRFRQEBIKENTKNDKQVOYIVKYT-SYDPDILLMKKSARNSCWSKDAEYGLYSI 204
DB 72 LYANICFRHHETSGSVPTDYQLQVMYVVKTSIKIPSSHNLMKGGSTKWSGSEPHFYSI 131
QY 205 YOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
DB 132 NVGGFFKLAGEEISIQVSNFSLDPPDQDQATYFGAFKV 169

RESULT 11

US-09-396-937-12
Sequence 12, Application US/09396937
Patent No. 6645500
GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: HAANING, Jesper
TITLE OF INVENTION: Method
TITLE OF INVENTION: Activity
FILE REFERENCE: 22021 PC 1
CURRENT APPLICATION NUMBER: US/09/396,937
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 173

```
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Fusion of
/ OTHER INFORMATION: murine OPG, residues 158-316 with C to S
/ OTHER INFORMATION: mutation, and His tag
US-09-396-937-12

Query Match      17.8%; Score 228.5; DB 4; Length 173;
Best Local Similarity 34.2%; Pred. No. 7.4e-16;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

QY 86 AHITGRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGFFY 145
DB 22 AHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKISNMTLSNGKLRVNDQGFY 71
QY 146 IYSQTYFRFQBEIKENTKNDKQMVQYIYKVT-SYPDPILLMKSAARNSCWSDAEVGLYSI 204
DB 72 LYANICFRHHTSGSVPTDYQLVMVYVVKTSIKIPSSHNLMMKGSTKQWNSGFHFYSI 131
QY 205 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFGAFV 242
DB 132 NVGGFFKLARAGEISIQVSNPSLLDPDQDATYFGAFKV 169

RESULT 12
US-09-396-937-8
/ Sequence 8, Application US/09396937
/ Patent No. 6645500
/ GENERAL INFORMATION:
/ APPLICANT: M&E Biotech A/S
/ APPLICANT: HALKIER, Torben
/ APPLICANT: HAANING, Jesper
/ TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
/ FILE REFERENCE: 22021 PC 1
/ CURRENT APPLICATION NUMBER: US/09/396,937
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 187
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR
/ OTHER INFORMATION: product with optimum codons for E. coli and P.
/ OTHER INFORMATION: pastoris expression
US-09-396-937-8

Query Match      17.8%; Score 228.5; DB 4; Length 187;
Best Local Similarity 34.2%; Pred. No. 8.3e-16;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

QY 86 AHITGRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGFFY 145
DB 36 AHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKISNMTLSNGKLRVNDQGFY 85
QY 146 IYSQTYFRFQBEIKENTKNDKQMVQYIYKVT-SYPDPILLMKSAARNSCWSDAEVGLYSI 204
DB 86 LYANICFRHHTSGSVPTDYQLVMVYVVKTSIKIPSSHNLMMKGSTKQWNSGFHFYSI 145
QY 205 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFGAFV 242
DB 146 NVGGFFKLARAGEISIQVSNPSLLDPDQDATYFGAFKV 183

RESULT 13
US-09-396-937-16
/ Sequence 16, Application US/09396937
/ Patent No. 6645500
/ GENERAL INFORMATION:
/ APPLICANT: M&E Biotech A/S
```

```
/ APPLICANT: HALKIER, Torben
/ APPLICANT: HAANING, Jesper
/ TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
/ FILE REFERENCE: 22021 PC 1
/ CURRENT APPLICATION NUMBER: US/09/396,937
/ CURRENT FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 182
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Fusion
/ OTHER INFORMATION: between murine OPG, residues 158-316 with tetanus
/ OTHER INFORMATION: toxoid P2 epitope introduced, and His tag
US-09-396-937-16

Query Match      16.3%; Score 210; DB 4; Length 182;
Best Local Similarity 32.0%; Pred. No. 6.6e-14;
Matches 55; Conservative 31; Mismatches 56; Indels 30; Gaps 6;

QY 86 AHITGRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGFFY 145
DB 22 AHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKISNMTLSNGKLRVNDQGFY 71
QY 146 IYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDPDPILLMK-----ARNS----- 191
DB 72 LYANICFRHHTSGSVPTDYQLVMVYVVK-----TPKIQSSHNLMMQYIKANSKFIGITE 126
QY 192 -CWSKDAFYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFGAFV 242
DB 127 LNWGSEFHFYSINVGGFKLARAGEISIQVSNPSLLDPDQDATYFGAFKV 178

RESULT 14
US-09-396-937-14
/ Sequence 14, Application US/09396937
/ Patent No. 6645500
/ GENERAL INFORMATION:
/ APPLICANT: M&E Biotech A/S
/ APPLICANT: HALKIER, Torben
/ APPLICANT: HAANING, Jesper
/ TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
/ FILE REFERENCE: 22021 PC 1
/ CURRENT APPLICATION NUMBER: US/09/396,937
/ CURRENT FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Fusion of
/ OTHER INFORMATION: murine OPG, residues 158-316 modified by
/ OTHER INFORMATION: introduction of tetanus toxoid P30 epitope, and
/ OTHER INFORMATION: His tag
US-09-396-937-14

Query Match      16.2%; Score 208; DB 4; Length 188;
Best Local Similarity 30.5%; Pred. No. 1.1e-13;
Matches 53; Conservative 34; Mismatches 59; Indels 28; Gaps 5;

QY 86 AHITGRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGFFY 145
DB 22 AHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKISNMTLSNGKLRVNDQGFY 71
QY 146 IYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDPDP-----IILMKSA 188
DB 72 LYANICFRHHTSGSVPTDYQLVMVYVVK-TSIKIPSSHNLMMFNNTVSWFLRVPKVSAS 130
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QY 189 RNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 242
Db 131 HLENWGSNSEPHFYSINVGPFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 184

RESULT 15

US-09-396-937-20
; Sequence 20, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANNING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion between
; OTHER INFORMATION: murine OPGL, residues 158-316 with tetanus toxoid
; OTHER INFORMATION: P30 epitope introduced, and His tag
US-09-396-937-20

Query Match 15.7%; Score 202.5; DB 4; Length 173;
Best Local Similarity 30.2%; Pred. No. 3.7e-13;
Matches 52; Conservative 28; Mismatches 53; Indels 39; Gaps 5;
QY 86 AHITGTRGRNLTSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLNGLVIEKGFYY 145
Db 22 AHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKISNMTLSNGKLRVNDQGFYY 71
QY 146 IYSQTYFR-----FQEIKNKDKOMQVYIKYTSYDPILLMKARN 190
Db 72 LYANICFNFTVGFMLRVPKVSASHLEVKTSLK-----IPSSHNLKGGST 117
QY 191 SCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 242
Db 118 KNWGSNSEPHFYSINVGPFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 169

Search completed: March 23, 2004, 09:16:23
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:15:19 ; Search time 43 Seconds
(without alignments)

1463.399 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYSGIACFL.....NEHLDMDEHASFGLVNG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 644882

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	887	68.9	168	9 US-09-900-530A-10	Sequence 10, Appl
2	878	68.2	166	9 US-09-779-050A-16	Sequence 16, Appl
3	859	66.7	164	13 US-10-116-378-29	Sequence 29, Appl
4	850	66.0	161	14 US-10-216-074-7	Sequence 7, Appl
5	849	66.0	161	14 US-10-338-083-11	Sequence 11, Appl
6	826	64.2	208	9 US-09-855-544A-16	Sequence 16, Appl
7	746.5	58.0	188	9 US-09-855-544A-14	Sequence 14, Appl
8	636	49.4	172	9 US-09-779-050A-17	Sequence 17, Appl
9	446	34.7	85	14 US-10-286-696-12	Sequence 12, Appl
10	370	28.7	113	9 US-09-855-544A-15	Sequence 15, Appl
11	291	22.6	98	9 US-09-855-544A-10	Sequence 10, Appl
12	278	21.6	56	15 US-10-399-018-20	Sequence 20, Appl
13	277	21.5	88	9 US-09-855-544A-9	Sequence 9, Appl
14	245.5	19.1	87	14 US-10-286-696-13	Sequence 13, Appl
15	236	18.3	178	15 US-10-338-785A-2	Sequence 2, Appl

16	233.5	18.1	199	12	US-10-289-456-86	Sequence 86, Appl
17	233.5	18.1	199	14	US-10-050-902-224	Sequence 224, Appl
18	233.5	18.1	199	14	US-10-050-898-224	Sequence 224, Appl
19	232.5	18.1	151	14	US-10-338-083-10	Sequence 10, Appl
20	232.5	18.1	158	12	US-10-289-456-101	Sequence 101, Appl
21	232.5	18.1	159	12	US-10-289-456-84	Sequence 84, Appl
22	232.5	18.1	160	9	US-09-779-050A-15	Sequence 15, Appl
23	232.5	18.1	165	12	US-10-289-456-103	Sequence 103, Appl
24	232.5	18.1	178	12	US-10-289-456-83	Sequence 83, Appl
25	232.5	18.1	180	12	US-10-289-456-100	Sequence 100, Appl
26	232.5	18.1	185	14	US-10-050-902-320	Sequence 320, Appl
27	232.5	18.1	185	14	US-10-050-898-320	Sequence 320, Appl
28	232.5	18.1	187	12	US-10-289-456-102	Sequence 102, Appl
29	230.5	17.9	170	10	US-09-791-153A-76	Sequence 76, Appl
30	230.5	17.9	193	12	US-10-289-456-96	Sequence 96, Appl
31	228.5	17.8	160	9	US-09-779-050A-14	Sequence 14, Appl
32	228.5	17.8	170	12	US-10-289-456-99	Sequence 99, Appl
33	190.5	14.8	213	14	US-10-185-425-2	Sequence 2, Appl
34	184.5	14.3	213	14	US-10-185-425-3	Sequence 3, Appl
35	177	13.8	159	14	US-10-185-425-1	Sequence 1, Appl
36	175.5	13.6	149	9	US-09-934-465-17	Sequence 17, Appl
37	175	13.6	34	14	US-10-272-411-24	Sequence 24, Appl
38	175	13.6	34	14	US-10-272-328A-24	Sequence 24, Appl
39	175	13.6	143	9	US-09-779-050A-8	Sequence 8, Appl
40	175	13.6	152	14	US-10-170-812-8	Sequence 5, Appl
41	173	13.4	138	14	US-10-216-074-5	Sequence 3, Appl
42	173	13.4	138	14	US-10-338-083-3	Sequence 30, Appl
43	173	13.4	140	13	US-10-116-378-30	Sequence 22, Appl
44	173	13.4	141	9	US-09-877-156-22	Sequence 7, Appl
45	173	13.4	143	9	US-09-779-050A-7	

ALIGNMENTS

RESULT 1

US-09-900-530A-10
; Sequence 10, Application US/09900530A
; Patent No. US20020128438A1
; GENERAL INFORMATION:
; APPLICANT: Seol, Dae-Wu
; APPLICANT: Billiar, Timothy R.
; TITLE OF INVENTION: DNA Cassette for the Production of
; Secretable Recombinant Trimeric Trail Proteins, Tetracycline
; Doxycycline-Inducible Adeno-Associated Virus Vector, Their
; TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated
; TITLE OF INVENTION: Combination and Use in Gene Therapy
; FILE REFERENCE: 5006-1-002
; CURRENT APPLICATION NUMBER: US/09/900.530A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: KR 2000-38441
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 168
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-900-530A-10

Query Match	68.9%	Score 887	DB 9	Length 168
Best Local Similarity	100.0%	Pred. No. 4.2e-77		
Matches 168	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	76	VREGPORVAHITGTGRSNTLSSPNKNEKALGRKINWESSRSGHSFLSNHLRNGE	135	
Db	1	VREGPORVAHITGTGRSNTLSSPNKNEKALGRKINWESSRSGHSFLSNHLRNGE	60	
QY	136	LVIHEKGFYIYSOTYFRFOEIKENTKNDQKQVOYIYKTYSDPDPILLMKASRNCWSK	195	
Db	61	LVIHEKGFYIYSOTYFRFOEIKENTKNDQKQVOYIYKTYSDPDPILLMKASRNCWSK	120	
QY	196	DAEYGLYSIOGGIFELKENDRIEVSVTNEHLDMDEHASFGLVNG	243	

Db 121 DABYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168

RESULT 2

US-09-779-050A-16
; Sequence 16, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-16

Query Match 68.2%; Score 878; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.1e-76;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 ERGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 137
Db 1 ERGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 60
QY 138 IHEKGFYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSARNCSWSDA 197
Db 61 IHEKGFYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSARNCSWSDA 120
QY 198 EYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 EYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 166

RESULT 3

US-10-116-378-29
; Sequence 29, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGY AND
; TITLE OF INVENTION: NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/116,378
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 29
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-29

Query Match 66.7%; Score 859; DB 13; Length 164;
Best Local Similarity 99.4%; Pred. No. 2e-74;
Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 80 GFORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 139
Db 1 GFORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 60
QY 140 EKGFFYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSARNCSWSDA 199
Db 61 EKGFFYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSARNCSWSDA 120
QY 200 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 164

RESULT 4

US-10-216-074-7
; Sequence 7, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-7

Query Match 66.0%; Score 850; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.4e-73;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 142
Db 1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 60
QY 143 FYIYISQTYFRFQEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSARNCSWSDA 202
Db 61 FYIYISQTYFRFQEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSARNCSWSDA 120
QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 5

US-10-338-083-11
; Sequence 11, Application US/10338083
; Publication No. US20030166559A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Basil I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-11

Query Match      66.0%; Score 849; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.8e-73;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 QVAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEK 141
Db 1 QVAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEK 60

Qy 142 GFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSWCKDAEYGL 201
Db 61 GFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSWCKDAEYGL 120

Qy 202 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 6
US-09-855-544A-16
; Sequence 16, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855.544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-16

Query Match      64.2%; Score 826; DB 9; Length 208;
Best Local Similarity 96.3%; Pred. No. 4.1e-71;
Matches 156; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVQWLRLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVQWLRLVRKMLRTSEE 98

Qy 61 TISTVQEKQONISPLVRERGQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVRERGQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHSFLNLHRLNGELVTHEKGFYYISQTYFRFOEIKENT 162
Db 159 SGHSFLNLHRLNGELVTHEKGFYYISQTYFRFOEIKENT 200

RESULT 7
US-09-855-544A-14
; Sequence 14, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855.544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-14

Query Match      58.0%; Score 746.5; DB 9; Length 188;
Best Local Similarity 61.7%; Pred. No. 1.5e-63;
Matches 150; Conservative 0; Mismatches 0; Indels 93; Gaps 1;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVQWLRLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVQWLRLVRKMLRTSEE 98

Qy 61 TISTVQEKQONISPLVRERGQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQ-----ENTKNDKQMVQIYKYTSYDP 104

Qy 121 SGHSFLNLHRLNGELVTHEKGFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDP 180
Db 105 -----ENTKNDKQMVQIYKYTSYDP 125

Qy 181 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 126 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 185

Qy 241 LVG 243
Db 186 LVG 188

RESULT 8
US-09-779-050A-17
; Sequence 17, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779, 050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-17

Query Match      49.4%; Score 636; DB 9; Length 172;
Best Local Similarity 71.4%; Pred. No. 5.6e-53;
Matches 120; Conservative 20; Mismatches 22; Indels 6; Gaps 1;

Qy 81 PQVAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEK 140
Db 4 PQVAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEK 63

Qy 141 KGFYYISQTYFRFOE-----IKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSW 194
Db 64 EGLYIYVSYQTYFRFOEADASKMVSKDKVTKQLVQIYKYTSYDPDPILLMKSARNCSW 123

Qy 195 KDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242
Db 124 RDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 171

RESULT 9
US-10-286-696-12
; Sequence 12, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
```

```
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm A No. US20030129706Alal Member of the TNF Ligand Supergene H
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-696-12

Query Match      34.7%; Score 446; DB 14; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.8e-35;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 ERGPQVAHITGRGRSNTLSSPNSKNEKALGRKINSMESSRSGHSLNHLRNGELV 137
Db 1 ERGPQVAHITGRGRSNTLSSPNSKNEKALGRKINSMESSRSGHSLNHLRNGELV 60

QY 138 IHEKGFYIYSQYFRPQBEIKENT 162
Db 61 IHEKGFYIYSQYFRPQBEIKENT 85

RESULT 10
US-09-855-544A-15
; Sequence 15, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-15

Query Match      28.7%; Score 370; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQLRQVLRKMLRTSEE 60
Db 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQLRQVLRKMLRTSEE 98

QY 61 TISTVQEQK 69
Db 99 TISTVQEQK 107

RESULT 11
US-09-855-544A-10
; Sequence 10, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 98
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-10

Query Match      22.6%; Score 231; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-20;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQLRQVLRK 52
Db 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQLRQVLRK 90

RESULT 12
US-10-399-018-20
; Sequence 20, Application US/10399018
; Publication No. US20040002118A1
; GENERAL INFORMATION:
; APPLICANT: Smilansky, Zeev
; TITLE OF INVENTION: METHOD FOR DETERMINING MASS ALTERING MOIETY IN PEPTIDES
; FILE REFERENCE: 9124.137USWO
; CURRENT APPLICATION NUMBER: US/10/399,018
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/IL01/00944
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: IL138946
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-018-20

Query Match      21.6%; Score 278; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 RTSEETISTVQEQKQNISPLVREGRPQVAAHITGRGRSNTLSSPNSKNEKALGR 111
Db 1 RTSEETISTVQEQKQNISPLVREGRPQVAAHITGRGRSNTLSSPNSKNEKALGR 56

RESULT 13
US-09-855-544A-9
; Sequence 9, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-9

Query Match      21.5%; Score 277; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 6.9e-19;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQLRQVLRK 49
Db 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQLRQVLRK 87

RESULT 14
US-10-286-696-13
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; Sequence 13, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. US20030129706A1 Member of the TNF Ligand Supergene F
; FILE REFERENCE: 01017/3550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mouse
US-10-286-696-13

Query Match 19.1%; Score 245.5; DB 14; Length 87;
Best Local Similarity 65.8%; Pred. No. 7.2e-16;
Matches 50; Conservative 9; Mismatches 14; Indels 3; Gaps 1;
QY 81 PORVAHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSPFLSNLHLRNGELVHIE 140
DB 4 POKVAHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSPFLSNLHLRNGELVHIE 140
QY 141 KGFYIYSQTYFRFQE 156
DB 64 E---YIYSQTYFRFQE 76

RESULT 15
US-10-338-785A-2
; Sequence 2, Application US/10338785A
; Publication No. US20030219864A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hubert, Rene S.
; APPLICANT: El Yazal, Jamal
; TITLE OF INVENTION: No. US20030219864A1 Variants of RANKL Protein
; FILE REFERENCE: A-71486
; CURRENT APPLICATION NUMBER: US/10/338,785A
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: construct of human RANKL extracellular region with histidine tag
; OTHER INFORMATION: and TEV protease cleavage site
US-10-338-785A-2

Query Match 18.3%; Score 236; DB 15; Length 178;
Best Local Similarity 32.7%; Pred. No. 1.6e-14;
Matches 55; Conservative 35; Mismatches 64; Indels 14; Gaps 5;
QY 79 RGPQVA---AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSPFLSNLHLRNGE 135
DB 17 QGPKEAQPFAHT-----INATDIPSGSHKVSLS---SSWYHDR-GWAKISNMTFSNCK 66
QY 136 LVIHKGFIYYSQTYFRFQEEIKENTKNDKQMVYIKYT-SYDPILLMKSNRSCWS 194
DB 67 LIVNQDGFYLYANICFRHHTSGDLATEYQLMWVYVTKTSIKIPSSHTLMKGGSTKYWS 126
QY 195 KDAEYGLYSIQGIGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 242

Db 127 GNSEPHFYISINVGGFFKLRSGEEISIEVSNPSSLDDPDODATYFGAFKV 174
Search completed: March 23, 2004, 09:20:56
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:07:23 ; Search time 60 Seconds
(without alignments)
1144.317 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287
Sequence: 1 INELKQMDKYSKGIACFL.....NEHLIDMDHEASFFGAFLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1166853

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	953.5	74.1	220	3	AAY88630 Cell fact
2	907	70.5	173	5	ABG72258 Partial h
3	887	68.9	168	4	ABG76826 Human TRF
4	887	68.9	168	5	Aau99896 Human TNF
5	882	68.5	168	5	ABG72259 Partial h
6	878	68.2	166	3	AAB08274 Amino aci
7	866	67.3	167	6	ABR84402 TPAIL ani
8	850	66.0	161	4	AAY71985 C-termina
9	850	66.0	161	6	ABR39855 TNF fam1
10	850	66.0	161	7	ADCO3335 Tumour ne
11	827	64.3	212	5	Aau99301 Human TRA
12	746.5	58.0	188	5	Aau79599 Human TRA
13	727	56.5	139	2	AAY01518 Polypepti
14	633	49.2	172	3	AAB08275 Amino aci
15	425	33.0	121	3	AAG03752 Human sec
16	370	28.7	113	5	Aau79600 Human TRA
17	291	22.6	98	5	Aau79595 Human TRA
18	291	22.6	101	2	AAM19790 Human apo
19	291	22.6	101	2	Aaw56761 Human TRA
20	291	22.6	101	4	AAE11032 Human TRA
21	291	22.6	101	6	ABU08559 Human TNF
22	278	21.6	56	5	AAE23263 Protein #
23	277	21.5	88	5	Aau79594 Human TRA
24	236	18.3	178	6	ADA50080 Human wil
25	233.5	18.1	199	5	ABG94285 Mouse RAN

26	233.5	18.1	199	5	ABG80597	Abg80597 Mouse rec
27	232.5	18.1	152	4	AA567248	Aab67248 Human RAN
28	232.5	18.1	160	3	AA808273	Aab08273 Amino aci
29	232.5	18.1	185	5	ABG94338	Abg94338 Human C-R
30	232.5	18.1	185	5	ABG80650	ABG80650 Human RAN
31	232.5	18.1	186	5	ABG71829	ABG71829 Human RAN
32	232.5	18.1	200	5	ABG71827	ABG71827 Human RAN
33	232.5	18.1	216	7	ADB16998	Aau16998 Human RAN
34	230.5	17.9	170	4	AAU08386	Aau08386 Mouse FLA
35	230.5	17.9	216	7	ADB16999	ADB16999 Murine RA
36	228.5	17.8	155	6	ABR39854	ABR39854 RANK liga
37	228.5	17.8	155	7	ADCO3334	ADCO3334 Murine re
38	228.5	17.8	160	3	AAH08272	Aab08272 Amino aci
39	228.5	17.8	173	3	AA844422	Aay844422 A murine
40	228.5	17.8	173	3	AA844421	Aay844421 Amino aci
41	228.5	17.8	187	3	AA844420	Aay844420 Amino aci
42	219	17.0	139	3	AA91023	Aay91023 Mouse OBM
43	210	16.3	182	3	AA844424	Aay844424 An osteop
44	208	16.2	188	3	AA844423	Aay844423 An osteop
45	202.5	15.7	173	3	AA844426	Aay844426 An osteop

ALIGNMENTS

RESULT 1

AA88630
ID AAY88630 standard; protein; 220 AA.

XX AC AAY88630;

DT 22-AUG-2000 (first entry)

DE Cell factor derivative TRAILD amino acid sequence.

XX Cell factor derivative; TRAILD; anticancer; cancer; liver; breast;
XX kidney; leukaemia.

OS Unidentified.

XX CN1243748-A.

PD 09-FEB-2000.

XX PF 28-JUL-1999; 99CN-00111039.

XX PR 28-JUL-1999; 99CN-00111039.

XX (BAST-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.

XX Zheng D, Liu Y, Ma Z;

XX WPI; 2000-351201/31.

XX New cell factor derivative causing cells to die, for anticancer therapy.

XX Disclosure; Page 2; 10pp; Chinese.

XX The present invention relates to a cell factor derivative (TRAILD) used as an anticancer derivative. The TRAIL protein can be expressed in soluble form in bacterial cytoplasm. The present sequence represents a TRAILD amino acid sequence. Recombinant TRAILD fusion proteins can be used in anti-cancer medicaments to treat cancer of the liver, breast, or kidney. It can also be used to treat leukaemia

XX Sequence 220 AA;

XX Query Match 74.1%; Score 953.5; DB 3; Length 220;

XX Best Local Similarity 97.9%; Pred. NO. 7.4e-85;

XX Matches 185; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

XX 56 RTSETITVQKQONISPLVREGRPORVAHITTCRGSRNTLSPNSKNEKALGRKINS 115

Db 32 KTSEETISTVQEKQONISPLVRRGQPVAAHITGTRGRSQTLSSPNSKNEKALGRKINS 91
 QY 116 WESSRSGHSLNHLRNGELVIH-BKGFYIYSQTYFRFOEIKENTKNDKQWQYIYK 174
 Db 92 WESSRSGHSLNHLRNGELVIHKEGFYIYSQTYFRFOEIKENTKNDKQWQYIYK 151
 QY 175 YTSYPPDILLMKSGARNSCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEA 234
 Db 152 YTSYPPDILLMKSGARNSCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEA 211
 QY 235 SFFGAFLVG 243
 Db 212 SFFGAFLVG 220

RESULT 2
 ID ABG72258
 XX ABG72258 standard; protein; 173 AA.
 AC ABG72258;
 XX
 DT 04-MAR-2003 (first entry)
 DE
 XX
 XX
 XX Partial human Trail protein, Trail109.
 XX Human; tumour related apoptosis inducing ligand; Trail109;
 XX Trail prokaryotic expression system; tumour cell death.
 XX Homo sapiens.
 XX
 XX
 XX Key Location/Qualifiers
 PH Misc-difference 109 /note= "Encoded by CTT"
 FT
 XX
 XX CN1354183-A.
 XX
 XX 19-JUN-2002.
 XX
 XX 30-NOV-2001; 2001CN-00132371.
 XX
 XX 30-NOV-2001; 2001CN-00132371.
 XX
 XX (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
 XX
 XX Hu Y, Yao Y;
 XX
 XX WPI; 2002-751439/82.
 XX N-PSDB; ABX14392.
 XX
 XX Tumor death induction ligand gene, gene expression protein and its
 XX preparation method.
 XX
 XX Claim 7; Page 10 (disclosure); 17pp; Chinese.
 XX
 XX The present invention relates to the isolation of cDNA encoding human
 XX tumour related apoptosis inducing ligand (Trail), and the Trail protein.
 XX The Trail full length cDNA is cloned, and is utilised to create a Trail
 XX prokaryotic expression system. The full length Trail cDNA is used to
 XX respectively clone cDNA of soluble ectocytic segment Trail109 and Trail
 XX 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic
 XX expression systems. The prokaryotic expression systems created greatly
 XX increase the expression and quantity of the Trail, Trail109, and Trail114
 XX proteins, and may be useful in a new preparation for killing tumour
 XX cells. The present sequence represents the partial human Trail protein,
 XX Trail109
 XX
 XX Sequence 173 AA;
 XX
 XX Query Match 70.5%; Score 907; DB 5; Length 173;
 XX Best Local Similarity 99.4%; Pred. No. 1.9e-80;
 XX Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 71 NISPLVRRGQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHL 130

Db 1 NISPLVRRGQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHL 60
 QY 131 LRNGELVIHKEGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSAEN 190
 Db 61 LRNGELVIHKEGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSAEN 120
 QY 191 SCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
 Db 121 SCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 173

RESULT 3
 ABB76826
 ID ABB76826 standard; protein; 168 AA.
 XX
 AC ABB76826;
 XX
 DT 16-JUL-2002 (first entry)
 DE
 XX
 XX Human TRAIL.
 XX Human; TRAIL; tumour necrosis factor; TNF;
 XX tumour necrosis factor related apoptosis inducing ligand; TRAIL; cancer;
 XX viral infection; cytostatic.
 XX Homo sapiens.
 XX
 XX KR2001019100-A.
 XX
 XX 15-MAR-2001.
 XX
 XX 25-AUG-1999; 99KR-00035354.
 XX
 XX 25-AUG-1999; 99KR-00035354.
 XX
 XX (DONG-) DONG WHA PHARM IND CO LTD.
 XX
 XX Cha SS, Kim JU, Lee GJ, Lim GM, Oh BH, Yoon JI, Yoon SJ;
 XX WPI; 2001-533833/59.
 XX N-PSDB; ABL53366.
 XX
 XX Producing and crystallizing tumor necrosis factor related apoptosis
 XX inducing ligand protein, and its three-dimensional structure.
 XX
 XX Claim 1; Page 14; 20pp; Korean.
 XX
 XX The present invention relates to a method for producing Tumour Necrosis
 XX Factor (TNF) Related Apoptosis Inducing Ligand (TRAIL) protein, and for
 XX crystallising the TRAIL protein and its three-dimensional structure,
 XX where the TRAIL protein has improved activity, which specifically kills
 XX cancer cells and cells infected by virus. The present sequence is human
 XX TRAIL, which was used in the invention
 XX
 XX Sequence 168 AA;
 XX
 XX Query Match 68.9%; Score 887; DB 4; Length 168;
 XX Best Local Similarity 100.0%; Pred. No. 1.6e-78;
 XX Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 76 VRRGQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 135
 Db 1 VRRGQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 60
 QY 136 LVTHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSAENSCWSK 195
 Db 61 LVTHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSAENSCWSK 120
 QY 196 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
 Db 121 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168

Db 121 DAHYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168

RESULT 5
ABG72259
ID ABG72259 standard; protein; 168 AA.
XX
AC ABG72259;
AC
DT 04-MAR-2003 (first entry)
XX
DE Partial human Trail protein, Trail114.
XX
KW Human; tumour related apoptosis inducing ligand; Trail114;
KW Trail prokaryotic expression system; tumour cell death.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 104
FT /note= "Encoded by CTT"
XX
PN CN1354183-A.
XX
PD 19-JUN-2002.
XX
PF 30-NOV-2001; 2001CN-00132371.
XX
PR 30-NOV-2001; 2001CN-00132371.
XX
PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
XX
PI Hu Y, Yao Y;
XX
DR WPI; 2002-751439/82.
DR N-PSDB; ABX14393.
XX
PT Tumor death induction ligand gene, gene expression protein and its
XX preparation method.
XX
PS Claim 7; Page 10 (disclosure); 17pp; Chinese.
XX
CC The present invention relates to the isolation of cDNA encoding human
CC tumour related apoptosis inducing ligand (Trail); and the Trail protein.
CC The Trail full length cDNA is cloned, and is utilised to create a Trail
CC prokaryotic expression system. The full length Trail cDNA is used to
CC respectively clone cDNA of soluble ectocytic segment Trail109 and Trail
CC 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic
CC expression systems. The prokaryotic expression systems created greatly
CC increase the expression and quantity of the Trail, Trail109, and Trail114
CC proteins, and may be useful in a new preparation for killing tumour
CC cells. The present sequence represents the partial human Trail protein,
CC Trail114
XX
SQ Sequence 168 AA;

Query Match 68.5%; Score 882; DB 5; Length 168;
Best Local Similarity 99.4%; Pred. No. 5.1e-78;
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 76 VRERGQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNRGE 135
Db 1 VRERGQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNRGE 60

QY 136 LVTHEKGFYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSK 195
Db 61 LVTHEKGFYIYSQTYFRQEEIKENAKNDKQVQIYKYTSYDPDPILLMKSARNCSWSK 120

QY 196 DAHYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 DAHYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168

```

XX AC ABR84402;
XX DT 09-OCT-2003 (first entry)
XX DE TRAIL amino acid sequence.
XX KW TRAIL; TNF-related apoptosis-inducing ligand; tumour; necrosis.
XX OS Unidentified.
XX PN CN1380339-A.
XX PD 20-NOV-2002.
XX PF 10-APR-2001; 2001CN-00105946.
XX PR 10-APR-2001; 2001CN-00105946.
XX PA (CHEN-) CHENGDU DIAO PHARM GROUP CO LTD.
XX PI Li B, Gao X, Liu Z;
XX DR WPI; 2003-230973/23.
XX DR N-PSDB; ACC83357.
XX PT Death induced ligand (TRAIL) cDNA and encoded polypeptide, useful for
XX PT inducing the death of tumor cells, is related to mutational human tumor
XX PT necrosis.
XX PS Claim 4; Fig 2; 14pp; Chinese.
XX CC The invention relates to a TNF-related apoptosis-inducing ligand encoding
XX CC (TRAIL) cDNA and its encoded polypeptide. The gene of the invention is
XX CC related to mutational human tumor necrosis. The polypeptide of the
XX CC invention is useful for inducing the death of tumor cells. The current
XX CC sequence represents the TRAIL amino acid sequence
XX SQ Sequence 167 AA;

Query Match 67.3%; Score 866; DB 6; Length 167;
Best Local Similarity 98.2%; Pred. No. 1.9e-76;
Matches 166; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 75 LVNERGPQVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNG 134
DB 1 MVRERG-RVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNG 58
QY 135 ELVIHEKGFYIYQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWS 194
DB 59 ELVIHEKGFYIYQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWS 118
QY 195 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 243
DB 119 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 167

RESULT 8
AAY71985
ID AAY71985 standard; protein; 161 AA.
XX AC AAY71985;
XX DT 28-MAR-2001 (first entry)
XX DE C-terminal region of human TRAIL protein.
XX KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
XX KW Tumour necrosis factor and Apol-related leucocyte expressed Ligand 1;
XX KW therapeutic; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
XX KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
XX KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
XX KW haemolytic anaemia; Grave's disease; myasthenia gravis; TRAIL protein;

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XX AC ABR84402;
XX DT 09-OCT-2003 (first entry)
XX DE TRAIL amino acid sequence.
XX KW TRAIL; TNF-related apoptosis-inducing ligand; tumour; necrosis.
XX OS Unidentified.
XX PN CN1380339-A.
XX PD 20-NOV-2002.
XX PF 10-APR-2001; 2001CN-00105946.
XX PR 10-APR-2001; 2001CN-00105946.
XX PA (CHEN-) CHENGDU DIAO PHARM GROUP CO LTD.
XX PI Li B, Gao X, Liu Z;
XX DR WPI; 2003-230973/23.
XX DR N-PSDB; ACC83357.
XX PT Death induced ligand (TRAIL) cDNA and encoded polypeptide, useful for
XX PT inducing the death of tumor cells, is related to mutational human tumor
XX PT necrosis.
XX PS Claim 4; Fig 2; 14pp; Chinese.
XX CC The invention relates to a TNF-related apoptosis-inducing ligand encoding
XX CC (TRAIL) cDNA and its encoded polypeptide. The gene of the invention is
XX CC related to mutational human tumor necrosis. The polypeptide of the
XX CC invention is useful for inducing the death of tumor cells. The current
XX CC sequence represents the TRAIL amino acid sequence
XX SQ Sequence 167 AA;

Query Match 67.3%; Score 866; DB 6; Length 167;
Best Local Similarity 98.2%; Pred. No. 1.9e-76;
Matches 166; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 75 LVNERGPQVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNG 134
DB 1 MVRERG-RVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNG 58
QY 135 ELVIHEKGFYIYQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWS 194
DB 59 ELVIHEKGFYIYQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWS 118
QY 195 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 243
DB 119 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 167

RESULT 8
AAY71985
ID AAY71985 standard; protein; 161 AA.
XX AC AAY71985;
XX DT 28-MAR-2001 (first entry)
XX DE C-terminal region of human TRAIL protein.
XX KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
XX KW Tumour necrosis factor and Apol-related leucocyte expressed Ligand 1;
XX KW therapeutic; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
XX KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
XX KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
XX KW haemolytic anaemia; Grave's disease; myasthenia gravis; TRAIL protein;

```


KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 2..8
 FT /label= Beta_strand.
 FT Region 32..34
 FT /label= Beta_strand
 FT Region 42..44
 FT /label= Beta_strand
 FT Region 47..50
 FT /label= Beta_strand
 FT Region 53..56
 FT /label= Beta_strand
 FT Region 61..72
 FT /label= Beta_strand
 FT Region 86..91
 FT /label= Beta_strand
 FT Region 99..109
 FT /label= Beta_strand
 FT Region 118..128
 FT /label= Beta_strand
 FT Region 133..143
 FT /label= Beta_strand
 FT Region 153..160
 FT /label= Beta_strand

XX WO200068378-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US012266.

XX 06-MAY-1999; 99US-0132892P.

XX 01-MAY-2000; 2000US-0201012P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Shu HS;

XX WPI; 2001-016094/02.

XX Isolated TALL-1 protein is used to identify compounds that regulate B
 FT lymphocyte proliferation, used to treat B lymphocyte associated
 FT autoimmune disorders.

XX Example 1; Fig 1b; 112pp; English.

XX The present invention relates to Tumour necrosis factor (TNF) and Apol-
 CC related leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
 CC proteins (including homologues), and their antibodies. The invention in
 CC particular relates to methods for regulating the interaction between TALL
 CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
 CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.
 CC TALL-1 protein is useful for identifying compounds that regulate B
 CC lymphocyte proliferation. It is also useful for treating B lymphocyte
 CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus
 CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
 CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
 CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
 CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
 CC corresponding nucleic acid sequence are also useful in diagnostic assays.
 CC The present sequence is a C-terminal region of human TRAIL protein, which
 CC has 20-25% sequence identity with the C-terminal region of human TALL-1
 CC protein extracellular domain. TRAIL protein is a TNF family member

XX Sequence 161 AA;

Query Match 66.0%; Score 850; DB 4; Length 161;
 Best Local Similarity 100.0%; Pred. No. 6.5e-75;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 RVAAHITGTRSGNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 142

Db 1 RVAAHITGTRSGNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 60

Qy 143 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAARNSCWSDAEYGLY 202

Db 61 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAARNSCWSDAEYGLY 120

Qy 203 SIYQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAFLVG 243

Db 121 SIYQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 9

ABR39855

ID ABR39855 standard; protein; 161 AA.

XX ABR39855;

AC 11-AUG-2003 (first entry)

DT TNF family member, TRAIL (1d4v) protein fragment.

DE RANK; receptor activator of necrosis factor kB; RANK ligand; RANKL;

XX RANK; receptor activator of necrosis factor kB; RANK ligand; RANKL;

XX tumour necrosis factor; TNF; TRAIL; cytokine.

XX Unidentified.

XX WO2003014077-A2.

XX 20-FEB-2003.

XX 09-AUG-2002; 2002WO-US025287.

XX 09-AUG-2001; 2001US-0311163P.

XX 22-MAR-2002; 2002US-00105057.

XX (BARN-) BARNES-JEWISH HOSPITAL.

XX Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;

XX WPI; 2003-256526/25.

XX Composition for identifying a compound with Receptor Activator of

XX Necrosis Factor kB, RANK modulating activity and for identifying RANK or

XX osteoprotegerin modulating compound, has a protein complex in crystalline

XX form.

XX Disclosure; Fig 3; 66pp; English.

XX The invention relates to a composition (I) comprising a protein complex

XX in crystalline form, where the complex comprises an amino acid sequence

XX of a Receptor Activator of Necrosis Factor kB (RANK) Ligand (RANKL)

XX ectodomain. (I) is useful for identifying a compound with RANK modulating

XX activity, and for identifying a RANK or ORG modulating compound. (I) is

XX useful to intelligently design mutants that have altered biological

XX properties and for identifying and/or designing compounds that bind RANK

XX as an approach towards developing new therapeutic agents. (I) is also

XX useful to computationally screen small molecule databases for chemical

XX entities or compounds that can bind in whole, or in part, to RANK or

XX RANKL. The present sequence represents a tumour necrosis factor (TNF)

XX family member, TRAIL (1d4v), used in a structural-based alignment study

XX of murine RANKL protein

XX Sequence 161 AA;

XX Query Match 66.0%; Score 850; DB 6; Length 161;

XX Best Local Similarity 100.0%; Pred. No. 6.5e-75;

XX Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 83 RVAAHITGTRSGNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 142

Db 1 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 60
 QY 143 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 202
 Db 61 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 120
 QY 203 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
 Db 121 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 161

RESULT 10
 ADC03335
 ID ADC03335 standard; protein; 161 AA.
 XX AC ADC03335;
 XX DT 18-DEC-2003 (first entry)
 XX DE Tumour necrosis factor family cytokine, TRAIL.
 XX KW RANKL ectodomain crystal complex; RANK; osteoprotegerin; OPG;
 KW bone-forming compound; tumour necrosis factor; TNF family; cytokine;
 KW TRAIL.
 XX OS Mus sp.
 XX PN US2003050223-A1.
 XX PD 13-MAR-2003.
 XX PF 09-AUG-2002; 2002US-00215446.
 XX PR 09-AUG-2001; 2001US-0311163P.
 XX PA (LAMJ/) LAM J.
 PA (ROSS/) ROSS F P.
 PA (TEIT/) TEITELBAUM S L.
 PA (NELS/) NELSON C A.
 PA (FREM/) FREMONT D H.
 XX PI Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;
 XX WPI; 2003-605763/57.
 XX Composition comprising crystalline receptor activator of NFkappaB (RANK)
 PT ligand ectodomain complex whose three-dimensional structural
 PT representation is useful for identifying RANK or osteoprotegerin
 PT modulating compound.
 XX PS Disclosure; Fig 3; 40pp; English.

The invention relates to a composition comprising a protein complex in
 CC crystalline form, where the complex comprises an amino acid sequence of a
 CC receptor activator of nuclear factor kappaB (NFkappaB) (RANK) ligand
 CC (RANKL) ectodomain. The three-dimensional structural representation of a
 CC RANKL ectodomain crystal complex, is useful for identifying a RANK or
 CC osteoprotegerin (OPG) modulating compound, and for identifying a compound
 CC with RANK modulating activity. The crystals permit the determination of
 CC the three-dimensional X-ray diffraction structure of the crystal-line
 CC polypeptide to high resolution. The atomic structure coordinates and
 CC structural information which comprises atomic structure coordinates and
 CC useful for identifying bone-forming compounds by methods which utilise
 CC the coordinates for solving the three-dimensional X-ray diffraction
 CC and/or solution structures of other proteins, including mutant forms, to
 CC high resolution. The structural information may also be used in a variety
 CC of molecular modeling and computer-based screening applications to, for
 CC example design mutants of the crystallized RANKL, its receptors, or a
 CC portion or fragment of RANKL or its receptors. The coordinates of RANKL
 CC crystal, or subsets of such structural coordinates of the RANKL crystal,
 CC are useful for designing or identifying candidate compounds capable of
 CC modulating RANK biological activity, and for identifying compounds which

CC mimic the capability of RANKL to bind RANK molecules, thereby activating
 CC the receptor. The present sequence represents the amino acid sequence of
 CC the tumour necrosis factor family cytokine, TRAIL.
 XX SQ Sequence 161 AA;
 Query Match 66.0%; Score 850; DB 7; Length 161;
 Best Local Similarity 100.0%; Pred. No. 6.5e-75;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 83 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 142
 Db 1 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 60
 QY 143 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 202
 Db 61 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 120
 QY 203 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
 Db 121 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 161

RESULT 11
 AAU99301
 ID AAU99301 standard; protein; 212 AA.
 XX AC AAU99301;
 XX DT 24-SEP-2002 (first entry)
 XX DE Human TRAIL splice variant 8, rpl-6-6, protein.
 XX KW Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
 KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
 KW TRAIL; apoptosis; programmed cell death; differentiation; development;
 KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
 KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
 KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
 KW chromosome 3q26; rpl-6-6.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Domain 1..16 /note= "Cytoplasmic domain"
 FT Domain 17..38 /note= "Transmembrane domain"
 FT Domain 39..212 /note= "Extracellular domain"
 FT Misc-difference 209 /note= "Encoded by in-frame stop codon"
 XX US2002061525-A1.
 XX PN 23-MAY-2002.
 XX PD 16-MAY-2001; 2001US-00855544.
 XX PR 16-MAY-2000; 2000IL-00136156.
 XX PA (YELI/) YELIN R.
 PA (KHOS/) KHOSRAVI R.
 PA (SAVI/) SAVITZKY K.
 XX PI Yelin R, Khosravi R, Savitzky K;
 XX WPI; 2002-479259/51.
 XX New splice variants of tumor necrosis factor-related apoptosis inducing
 PT ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat
 PT diseases or disorders associated with low expression of the variants.
 XX

PS Claim 4; Fig 8; 29pp; English.

XX The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumor necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms. Apoptosis is induced by certain cytokines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1 and DcR2, lacking the intracellular signalling death domain. TRAIL, induced by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity. Determining these factors could provide possible mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polynucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of the TRAIL variant products. Diseases that may be treated include cancer, neurodegenerative diseases, autoimmune diseases, diseases involved in the non-normal development of tissues and aging. TRAIL's gene is located on chromosome 3q26. The sequence presented is the human TNF-related apoptosis inducing ligand (TRAIL) splice variant 8, rpi-6-6, protein which has had an C-terminal section of the conserved TNF domain deleted

XX Sequence 212 AA;

Query Match 64.3%; Score 827; DB 5; Length 212;
Best Local Similarity 91.3%; Pred. No. 1.7e-72;
Matches 159; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGTACFLKEDDSYWDNDDESNMSPCQVQKQRLVVKRMILRTSEE 60
Db 39 TNELKQMDKYSKSGTACFLKEDDSYWDNDDESNMSPCQVQKQRLVVKRMILRTSEE 98
QY 61 TISTVQEKQNI SPLVRERGPQVAAHITGTRGKSNLTSPNKGKALGRKINSWESSR 120
Db 99 TISTVQEKQNI SPLVRERGPQVAAHITGTRGKSNLTSPNKGKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIHKGFIYYSQYFRFQBEIKENTKNDKQMVQYIY 173
Db 159 SGHSFSLNHLRNGELVIHKGFIYYSQYFRFQBEIKENTKNDKQMVQYIY 211

RESULT 12
AAU79599
ID AAU79599 standard; protein; 188 AA.
XX AAU79599;
AC
XX
XX
DT 24-SEP-2002 (first entry)
XX
DE Human TRAIL splice variant 6, TRA-33-T7, protein.
XX Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
KW TRAIL; apoptosis; programmed cell death; differentiation; development;
KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
KW chromosome 3q26; TRA-33-T7.
XX

OS Homo sapiens.

XX Key Location/Qualifiers
FH Domain 1..16 /note= "Cytoplasmic domain"
FT Domain 17..38 /note= "Transmembrane domain"
FT Domain 39..188 /note= "Extracellular domain"
XX US2002061525-A1.
XX 23-MAY-2002.
XX 16-MAY-2001; 2001US-00855544.
XX 16-MAY-2000; 2000IL-00136156.
XX (YELI/) YELIN R.
XX (KHOS/) KHOSRAVI R.
XX (SAVI/) SAVITZKY K.
XX Yelin R, Khosravi R, Savitzky K;
XX WPI; 2002-479259/51.
XX New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.
XX Claim 4; Fig 9; 29pp; English.
XX The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumor necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms. Apoptosis is induced by certain cytokines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1 and DcR2, lacking the intracellular signalling death domain. TRAIL, induced by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity. Determining these factors could provide possible mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polynucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of the TRAIL variant products. Diseases that may be treated include cancer, neurodegenerative diseases, autoimmune diseases, diseases involved in the non-normal development of tissues and aging. TRAIL's gene is located on chromosome 3q26. The sequence presented is the human TNF-related apoptosis inducing ligand (TRAIL) splice variant 6, TRA-33-T7, protein which has had an N-terminal section of the conserved TNF domain deleted

XX Sequence 188 AA;
Query Match 58.0%; Score 746.5; DB 5; Length 188;
Best Local Similarity 61.7%; Pred. No. 1.1e-64;
Matches 150; Conservative 0; Mismatches 0; Indels 93; Gaps 1;
QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDNDDESNMSPCQVQKQRLVVKRMILRTSEE 60

Db 39 TNELKQWQDYKSKGIACFLKEDDSYWDPNDESSMNSPCWQVKWQLRQKMLRTSEE 98
QY 61 TISTVQEQQNI SPLVRRGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQ----- 104
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQYIYKTSYD 180
Db 105 -----ENTKNDKQMVQYIYKTSYD 125
QY 181 PILLMKARSNSCKDAEYGLYSIQGGIPELKENDRIFVSVTNEHLIDMDHEASFGAF 240
Db 126 PILLMKARSNSCKDAEYGLYSIQGGIPELKENDRIFVSVTNEHLIDMDHEASFGAF 185
QY 241 LVG 243
Db 186 LVG 188
RESULT 13
ID AAY01518
XX AAY01518 standard; peptide; 139 AA.
AC AAY01518;
XX
XX 27-MAY-1999 (first entry)
XX DT
XX DE
XX DE Polypeptide of the invention.
XX KW Neurodegenerative disease; autoimmune disease; inflammatory disease;
XX KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
XX KW surface receptor; TRAIL protein.
XX OS Homo sapiens.
XX
XX PN FR2766713-A1.
XX PD
XX PF 05-FEB-1999.
XX PF 04-AUG-1997; 97FR-00010176.
XX PR 04-AUG-1997; 97FR-00010176.
XX PA (INMR) BIO MERIEUX.
XX PI Rieger F, Belliveau JF, Perron H;
XX WPI; 1999-156177/14.
XX Use of polypeptide derived from TRAIL protein for diagnosis of
PT degenerative disease - autoimmunity and inflammation, also useful in
PT prevention or treatment, and similar use of corresponding ligand and
PT nucleic acid.
XX
XX Claim 5; Page 14; 21pp; French.
XX The specification describes the use a polypeptide corresponding to at
CC least the primary sequence of part AAY01516-17 to produce a diagnostic,
CC prophylactic or therapeutic composition useful in cases of degenerative,
CC autoimmune and inflammatory diseases. The polypeptides can be used in
CC treatment of neurodegenerative diseases, lupus erythematosus, rheumatoid
CC arthritis, and SEP. The polypeptides are apoptotic in central nervous
CC system cells, antigenic and specifically recognise the surface receptor
CC of the TRAIL protein. The polypeptide is a marker of disease and a
CC therapeutic target, e.g. its apoptotic activity can be blocked with an
CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
CC receptors, inhibiting formation of natural complex. The present sequence
CC represents a polypeptide of the invention
XX Sequence 139 AA;
SQ Query Match 56.5%; Score 727; DB 2; Length 139;

Best Local Similarity 100.0%; Pred. No. 5.9e-63;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 57 TSEETISTVQEQQNI SPLVRRGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 116
Db 1 TSEETISTVQEQQNI SPLVRRGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 60
QY 117 ESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQYIYK 176
Db 61 ESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQYIYK 120
QY 177 SYDPDPILLMKARSNSCKSK 195
Db 121 SYDPDPILLMKARSNSCKSK 139
RESULT 14
ID AAB08275
XX AAB08275 standard; protein; 172 AA.
AC AAB08275;
XX
XX 04-DEC-2000 (first entry)
XX DT
XX DE Amino acid sequence of a mouse TNF ligand TRAIL.
XX KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
XX KW type II transmembrane protein; B cell stimulatory factor;
XX KW inflammatory disorder; immune disorder; rheumatoid arthritis;
XX KW lupus and graft versus host disease.
XX OS Mus sp.
XX PN WO200047740-A2.
XX PD 17-AUG-2000.
XX PF 11-FEB-2000; 2000WO-US003653.
XX PR 12-FEB-1999; 99US-0119906P.
XX PR 18-NOV-1999; 99US-0166271P.
XX PA (AMGE-) AMGEN INC.
XX PI Boyle WJ, Hsu H;
XX WPI; 2000-558217/51.
XX Novel polypeptides comprising tumor necrosis factor ligand family
PT proteins, useful for treating inflammatory and immune disorders, e.g.
PT rheumatoid arthritis.
XX Claim 14; Fig 9; 71pp; English.
XX AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
CC specification describes an AGP-3 polypeptide, which is TNF ligand family
CC member. AGP-3 is a type II transmembrane protein, and is a potent B cell
CC stimulatory factor. Expression of AGP-3 correlates to increases in the
CC number of B cells and immunoglobulins produced. AGP-3 proteins,
CC antibodies, and nucleic acids may be used to treat inflammatory and
CC immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and
CC graft versus host disease. The nucleic acids may be used to regulate the
CC expression of an AGP-3 related protein. The AGP-3 proteins, antibodies
CC and nucleic acids are also useful for the detection of AGP-3 agonists,
CC antagonists and characterizing interactions with AGP-3 related proteins
XX SQ Sequence 172 AA;
Query Match 49.2%; Score 633; DB 3; Length 172;
Best Local Similarity 71.4%; Pred. No. 1.3e-53;
Matches 120; Conservative 20; Mismatches 22; Indels 6; Gaps 1;
QY 81 PQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHE 140

```
Db 4 PQVAAHITGTRRSNALIPISKDGTGKLGQKIESWESSRKGHSFLNHLVPRNGELVIEQ 63
QY 141 KGFVYYSQYFFFOEB-----IKENTKNDKQWQVYKYVTSYDPDPILLMKSGARNSCWS 194
Db 64 EGYLYYSQYFFFOEAEADASKVSKDKVTKQLVQYIYKTSYDPDPFVLKMGARNSCWS 123
QY 195 KDAEYGLYSYQGGIFELPKENDRIFVSVTNEHLMDHEASFFGAFV 242
Db 124 RDAEYGLYSYQGGIFELPKENDRIFVSVTNEHLMDLQDEASFFGAFV 171
```

RESULT 15

AAG03752
ID AAG03752 standard; protein; 121 AA.

XX AC AAG03752;

DT 06-OCT-2000 (first entry)

XX Human secreted protein, SEQ ID NO: 7833.

DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.

XX Homo sapiens.

OS Homo sapiens.

XX PN EP1033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 2000EP-00200610.

XX PR 26-FEB-1999; 99US-0122487P.

XX PA (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

DR N-PSDB; AAC03758.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 7833; 71pp + Sequence Listing; English.

PS The present sequence is a polypeptide encoded by one of a large number of

XX 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were

CC prepared from total human RNAs or polyA+ RNAs derived from 30 different

CC tissues. EST sequences usually correspond mainly to the 3' untranslated

CC region (UTR) of the mRNA because they are often obtained from oligo-dT

CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA

CC sequences derived from the 5' ends of mRNAs and even in those cases where

CC longer cDNA sequences have been obtained, the full 5' UTR is rarely

CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can

CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs

CC are also used in diagnostic, forensic, gene therapy and chromosome

CC mapping procedures. They are used to obtain upstream regulatory sequences

CC and to design expression and secretion vectors

XX Sequence 121 AA;

Query Match 33.0%; Score 425; DB 3; Length 121;

Best Local Similarity 100.0%; Pred. No. 1.8e-33;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRKMILRTSEE 60

Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRKMILRTSEE 98

QY 61 TISTVQEKQONISPLVREG 80

Db 99 TISTVQEKQONISPLVREG 118

Search completed: March 23, 2004, 09:13:49
Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:11:39 ; Search time 20 Seconds
(without alignments)
1168.727 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287
Sequence: 1 TNELKQMDKYSKSIACFL.....NEHLIDMDHDSFGAFLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 125680

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*

1: Piri.*
2: Piri2.*
3: Piri3.*
4: Piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134.5	10.5	204	1 S17289	tumor necrosis fac
2	131.5	10.2	234	1 A25451	tumor necrosis fac
3	130	10.1	232	1 S12606	tumor necrosis fac
4	129.5	10.1	235	1 I54490	tumor necrosis fac
5	127.5	9.9	204	1 S24641	lymphotoxin - bovi
6	126	9.8	234	1 JQ1344	tumor necrosis fac
7	123	9.6	233	1 QWHUN	tumor necrosis fac
8	122	9.5	205	1 QWHUX	lymphotoxin alpha
9	121	9.4	235	1 QWMSN	tumor necrosis fac
10	121	9.4	235	2 JU0029	tumor necrosis fac
11	120	9.3	233	1 S22052	tumor necrosis fac
12	117.5	9.1	234	1 JH0529	tumor necrosis fac
13	115.5	9.0	193	2 S06192	tumor necrosis fac
14	114	8.9	202	1 S27303	tumor necrosis fac
15	113.5	8.8	185	2 S52715	tumor necrosis fac
16	113	8.8	233	1 S24642	tumor necrosis fac
17	111.5	8.7	202	1 JN0869	tumor necrosis fac
18	107	8.3	197	1 JH0309	tumor necrosis fac
19	98.5	7.7	233	2 S11688	tumor necrosis fac
20	80.5	6.3	203	2 C89803	hypothetical prote
21	78	6.1	202	2 A82076	conserved hypotet
22	77	6.0	223	2 H71485	hypothetical prote
23	76.5	5.9	195	2 S77753	peptide transport
24	75.5	5.9	142	2 B87569	dnak suppressor pr
25	74	5.7	201	2 E82910	hypothetical prote
26	73	5.7	223	2 B64396	hypothetical prote
27	73	5.7	227	2 E70438	hypothetical prote
28	72.5	5.6	112	2 AF0347	conserved hypotet
29	72.5	5.6	123	2 T26862	hypothetical prote

30	72.5	5.6	156	2 H71623	probable secreted
31	72.5	5.6	218	2 A99014	hypothetical prote
32	72.5	5.6	243	2 A93387	sam-dependent meth
33	71.5	5.6	195	1 I40422	conserved hypotet
34	71.5	5.6	227	2 H64336	formate dehydrogen
35	71	5.5	234	2 T21543	hypothetical prote
36	70.5	5.5	189	2 D45188	chitin synthase (E
37	70.5	5.5	222	2 T37839	hypothetical prote
38	70.5	5.5	226	2 C81749	conserved hypotet
39	70	5.4	209	2 D90593	lipoprotein limpor
40	69.5	5.4	144	2 H81292	hypothetical prote
41	69.5	5.4	199	2 JE0351	OX40 ligand protei
42	69.5	5.4	201	2 S53800	chitin synthase (E
43	69.5	5.4	202	2 B90180	ABC transporter, A
44	69.5	5.4	222	2 A81896	hypothetical prote
45	69	5.4	139	2 T28300	ORF MSV139 hypotet

ALIGNMENTS

RESULT 1

S17289

tumor necrosis factor beta precursor - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: S17289

R/Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.

Gene 102, 171-178, 1991

A/Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative an

A/Reference number: S17289; MUID:91340150; PMID:1874444

A/Accession: S17289

A/Molecule type: DNA

A/Residues: 1-204 <KUH>

A/Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133

A/Genetics: 32/3; 68/1

A/Introns: 32/3; 68/1

C/Superfamily: tumor necrosis factor

C/Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

F/1-33/Domain: signal sequence #status predicted <SIG>

F/34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match 10.5%; Score 134.5; DB 1; Length 204;
Best Local Similarity 24.7%; Pred. No. 0.00037;
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;

QY 63 STVQEKQNMISPLVRERGPQVAAHTG-----TRGRSNTLSSPNSKNEKALGRKINS 115

Db 42 SAAQPAHQH-PPKHLARGTLKPAHLVGDPTSDLRWRANT-----DRAFLR---- 88

QY 116 WESSRSGHFLSNLHRLNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY 175

Db 89 -----HGFL-----LSNNLSLVPTSLGYFVYSQVVSFGEGCFPKATPTPLYLAHEVQLF 137

QY 176 TS-YPPDILLMKSAARNSCWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEA 234

Db 138 SSQYFPHVLLSAQKSCVCPQGPW-VRSVYQGAFLLTQGDQLSTHTDGTPLLHSPSS 196

QY 235 SFFGAF 240

Db 197 VFFGAF 202

RESULT 2

A25451

tumor necrosis factor alpha precursor - rabbit

N/Alternate names: cachectin; TNF alpha

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C/Accession: A25451; J50727

R/Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H

DNA 5, 149-156, 1986

A/Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for ra

A;Reference number: A25454; MUID:86219711; PMID:3519137
 A;Accession: A25454
 A;Molecule type: mRNA
 A;Residues: 1-234 <ITO>
 A;Cross-references: GB:W12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
 R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
 DNA 5, 157-165, 1986
 A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
 A;Reference number: A25451; MUID:86219712; PMID:3519138
 A;Accession: A25451
 A;Molecule type: DNA
 A;Residues: 1-234 <IT2>
 A;Note: this sequence differs from that shown in having a Gln inserted between residues
 R;Shakhov, A.N.; Kuprash, D.V.; Aizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
 Gene 95, 215-221, 1990
 A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
 A;Reference number: JH0309; MUID:91065534; PMID:2249779
 A;Accession: JS0727
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-62, 'Q', 63-234 <SHA>
 A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
 C;Genetics:
 A;Introns: 62/3; 80/1; 96/1
 A;Superfamily: tumor necrosis factor
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
 F;1-81/Domain: propeptide #status predicted <PRO>
 F;82-234/Product: tumor necrosis factor #status predicted <MAT>
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;147-178/Disulfide bonds: #status predicted

Query Match 10.2%; Score 131.5; DB 1; Length 234;
 Best Local Similarity 22.9%; Pred. No. 0.00079;
 Matches 50; Conservative 36; Mismatches 79; Indels 53; Gaps 10;

QY 29 PNDESMNSFCWQKWLQRLVKMI-LRTSEETISVQEKQNIPLVYRERGPQVAAH 87
 DB 58 PQEESPNN-----LHLNPNVQMVLTLSASALSD-----KPL-----AH 93
 QY 88 ITGTGRGNTLSSPNSKNEKALGRKINSWSSRSGHSFLSNLHRLNGELVHKEGFYIY 147
 DB 94 VVA-----NPQVEQL-----QWLSQRANALLANGMKLTQNLVVPADGLYLY 137
 QY 148 SQYFRFOBEIKENTKNDKQMVYIKY-TSYDDPILLMKARSNCWSKDAEYV-----L 201
 DB 138 SQVLFSGQ-----GCRSYVLLTHTVSRFAVSYPNKNVLLSAIKSPCHRETPPEAEPMAWY 192
 QY 202 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-PFG 238
 DB 193 EPIYLGGVFQLEKDRLLSTVNGPEYLDLAEISQVYFG 230

RESULT 3
 S12606
 tumor necrosis factor alpha precursor - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C;Accession: S12606; S17290; S18965; I46659
 R;Brews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
 Nucleic Acids Res. 18, 5564, 1990
 A;Title: Gene sequence of porcine tumor necrosis factor alpha.
 A;Reference number: S12606; MUID:91016861; PMID:2216741
 A;Accession: S12606
 A;Molecule type: DNA
 A;Residues: 1-232 <DRE>
 A;Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136
 R;Kuhnert, P.; Wuehrlich, C.; Peterhans, E.; Pauli, U.
 Gene 102, 171-178, 1991
 A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
 A;Reference number: S17289; MUID:91340150; PMID:1874444
 A;Accession: S17290
 A;Molecule type: DNA

A;Residues: 1-232 <KHU>
 A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
 A;Note: the authors translated the codon GAG for residue 202 as Gly
 R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
 submitted to the EMBL Data Library, January 1991
 A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis f
 A;Reference number: S18965
 A;Accession: S18965
 A;Molecule type: mRNA
 A;Residues: 1-232 <CHO>
 A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
 R;Pauli, U.; Beutler, B.; Peterhans, E.
 Gene 81, 185-191, 1989
 A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reactio
 A;Reference number: I46659; MUID:90034181; PMID:2478420
 A;Accession: I46659
 A;Status: preliminary; translated from GB/EMBL/DBBJ
 A;Molecule type: mRNA
 A;Residues: 44-232 <PAU>
 A;Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
 C;Genetics:
 A;Introns: 62/3; 78/1; 93/1
 C;Superfamily: tumor necrosis factor
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myr
 F;1-77/Domain: propeptide #status predicted <PRO>
 F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;144-176/Disulfide bonds: #status predicted

Query Match 10.1%; Score 130; DB 1; Length 232;
 Best Local Similarity 25.1%; Pred. No. 0.0011;
 Matches 43; Conservative 30; Mismatches 78; Indels 20; Gaps 6;

QY 80 GPORVAAHITGRGNTLSSPNS---KNEKALGRKINSWSSRSGHSFLSNLHRLNGEL 136
 DB 66 GLSLINPLAQGLRSSQTSQSKFAHVAVNVKAEGL--QWQSGYANALLANGVKLKDQNL 123
 QY 137 VTHEKGFYIYQTVFRFOEIKEN---TKNDKQMVYIKYTSYDDPILLMKARSNCW 193
 DB 124 VVPTDGLYLYSQVLFRGQCPSTNVFLTHTTSRIA-----VSQTKVNLLSAISKSPQ 177
 QY 194 SK-----DAEYGLYIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-PFG 238
 DB 178 RETPEGAEAKPWYFIYLGGVFQLEKDRLSAEINLPDYLDFAESGQVYFG 228

RESULT 4
 I54490
 tumor necrosis factor alpha precursor - white-footed mouse
 C;Species: Peromyscus leucopus (white-footed mouse)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
 C;Accession: I54490
 R;Crew, M.D.; Filipowsky, M.E.
 Immunogenetics 35, 351-353, 1992
 A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leu
 A;Reference number: I54490; MUID:92218012; PMID:1348497
 A;Accession: I54490
 A;Status: preliminary; translated from GB/EMBL/DBBJ
 A;Molecule type: DNA
 A;Residues: 1-235 <RES>
 A;Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
 C;Genetics:
 A;Gene: PLTNF
 A;Introns: 62/3; 81/1; 97/1
 C;Superfamily: tumor necrosis factor
 C;Keywords: glycoprotein; lipoprotein; myristylation
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 10.1%; Score 129.5; DB 2; Length 235;
 Best Local Similarity 24.5%; Pred. No. 0.0012;
 Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;

[illegible]

RESULT 7

QWJUN

tumor necrosis factor alpha precursor [validated] - human

C;Species: Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000

C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; I

R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica,

Nucleic Acids Res. 13, 6361-6373, 1985

A;Title: Human lymphotxin and tumor necrosis factor genes: structure, homology and cl

A;Reference number: A93585, MUID:86016093; PMID:2995927

A;Accession: A93585

A;Molecule type: DNA

A;Residues: 1-233 <NED>

A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210

R;Iris, F.J.M.; Bouquelier, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Ju

Nature Genet. 3, 137-145, 1993

A;Title: Dense lru clustering and a potential new member of the NFkappaB family withi

A;Reference number: S36152; MUID:93272029; PMID:8499947

A;Accession: S36153

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-233 <RI>

A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992

R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M,

Nature 312, 724-729, 1984

A;Title: Human tumour necrosis factor: precursor structure, expression and homology to

A;Reference number: A93351; MUID:85086244; PMID:6392892

A;Accession: A93351

A;Molecule type: mRNA

A;Residues: 1-233 <PEN>

A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210

A;Note: this protein was isolated from the monocyste-like cell line HL-60 from a promye

R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.

Science 228, 149-154, 1985

A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.

A;Reference number: A44189; MUID:85142190; PMID:3856324

A;Accession: A44189

A;Molecule type: mRNA

A;Residues: 1-62, 'S', 64-233 <WAN>

	Query Match	9.6%;	Score 123;	DB 1;	Length 233;	
	Best Local Similarity	23.0%;	Miscl. No. 0.0042;			
	Matches	43;	Conservative	32;	Mismatches 70;	Indels 42; Gaps 8;
QY	80 GPQR-----VAAHITGTRGSNTLSPNSK-----NEKALGRKINSWESSRGH	123				
Ddb	57 GPQREEPRDLISLPQAQRSSRT---PSDKPVAHVVFANFOAQO---CMLNRRANA	111				
QY	124 SFLSNLHLRNGELVIEHKGFYIYSQYPRFQEIKENTKNQKMVQVIYYKYT-----S	177				
	112 TAACTCTPRNQAVDPSEGVYIVTSQVLFVGO-----GCPSTHVLHTHSIRIAVS	162				

QY 178 YDPDILLMKSAARNCSWK-----DAEYGLYSIVQGIFELKENDRIAFVSVTNEHLIDMDH 232

DB 163 YQTKNVLISAISKPCQRTPEGAEAKPWEPYILGVGFQLEKGDRLSAEINRPDYLDFAE 222

QY 233 EAS-PFG 238
:
||

DB 223 SQGVTFG 229
:
||

RESULT 8

OWHX

Lymphotoxin alpha precursor - human

N;Alternate names: lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)

C;Species: Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000

R;Accession: A92755; S36154; I54482; A93350; B32877; A91906; A61478; S26951; A2

R;Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.; Goeddel

J. Cell. Biochem. 29, 171-181, 1985

A;Title: Structure and chromosomal localization of the human lymphotoxin gene.

A;Reference number: A92755; MUID:86086150; PMID:3001109

A;Accession: A92755

A;Molecule type: DNA

A;Residues: 1-59,'N','61'-205 <NED>

R;Iris, F.J.M.; Bougueret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurk

Nature Genet. 3, 137-145, 1993

A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within

A;Reference number: S36154; MUID:93272029; PMID:8499947

A;Accession: S36154

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-12,'R','14'-205 <IRI>

A;Cross-references: EMBL:Z15026; NID:937211; PID:CXA78746.1; PID:G37213

A;Note: The nucleotide sequence was submitted to the EMBL Data Library, August 1992

R;Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.

Immunogenetics 33, 50-53, 1991

A;Title: Haplotypic polymorphisms of the TNFB gene.

A;Reference number: I54482; MUID:91139175; PMID:1671667

A;Accession: I54482

A;Status: translation not shown; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-124,'P','126'-205 <RES>

A;Cross-references: GB:M55913; NID:G339742; PID:AAB59455.1; PID:G339743

A;Experimental source: ancestral haplotype 57.1

A;Note: 59-Asn was also found (ancestral haplotype 8.1)

R;Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.; Jarrett, J.A

Nature 312, 721-724, 1984

A;Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumour

A;Reference number: A93350; MUID:85086243; PMID:6334807

A;Accession: A93350

A;Molecule type: mRNA

A;Residues: 1-205 <GRA>

A;Cross-references: GB:X01393; NID:G34444; PID:CXA25649.1; PID:G34445

A;Experimental source: lymphoblastoid cell line RWI-1788

R;Goedel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M.F

Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986

A;Title: Tumor necrosis factors: gene structure and biological activities.

A;Reference number: A32877; MUID:87217059; PMID:3472740

A;Accession: B32877

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 35-205 <GOE>

R;Kobayashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T.

J. Biochem. 100, 727-733, 1986

A;Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell

A;Reference number: A91906; MUID:87057135; PMID:3536896

A;Accession: A91906

A;Molecule type: mRNA

A;Residues: 1-59,'N','61'-205 <KOB>

A;Cross-references: GB:D00102; NID:G219913; PID:BAA00064.1; PID:G219914

A;Note: The authors translated the codon TAT for residue 156 as Thr and ACC for resid

R;Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Masaki, N.; Nakamura, K.I.;

Lymphokine Res. 7, 175-185, 1988

A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A;Reference number: A61478; MUID:88301617; PMID:2841543
A;Accession: A61478
A;Molecule type: protein
A;Residues: 56-79;86-95,'X','97','X','99';119-151,'XX',154-162,'X',164,'X',166,'X',168,'X',1 R;Voigt, C.G.; Maurer-Pogoy, I.; Adolf, G.R.
FEBS Lett. 314, 85-88, 1992
A;Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylation A;Reference number: S26951; MUID:93083656; PMID:1451807
A;Accession: S26951
A;Molecule type: protein
A;Residues: 35-59,'N',61-205 <VOI>
A;Note: 60-Thr was also found
R;Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.
Arch. Biochem. Biophys. 304, 144-153, 1993
A;Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO A;Reference number: S34742; MUID:93311195; PMID:8323280
A;Contents: annotation
C;Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction, while having no detrimental effect on normal cells. It can also act synergistically with C;Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of different activities but are produced by different cell types and have different induction kinetics
C;Genetics:
A;Gene: GDB:LTA; LT: TNF
A;Cross-references: GDB:120442; OMIM:153440
A;Map position: 6p21.3-6p21.3
A;Introns: 33/3; 69/1
A;Note: The first intron occurs before the initiator codon
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage F;1-34/DNA: signal sequence #status predicted <SIG>
F;3-205/Product: lymphotoxin #status predicted <MAT>
F;41/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F;96/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 9.58; Score 122; DB 1; Length 205;
Best Local Similarity 23.48; Pred. No. 0.0043;
Matches 37; Conservative 29; Mismatches 72; Indels 20; Gaps 5;
A;Accession: S34742; MUID:93311195; PMID:8323280

QY 85 AAHTGTGRSNTLSNPSNKAALGRKINSWESSGHSFLSNLHNLNGELVHEKGFY 144
DB 64 AAHLIGDPKQNSL-----LWRANTDRAFLQDFSLNSNLLVPTSGIY 107

QY 145 YIVSQTVFRQBEIKENTKNDKQMVQIYKYS-YPDPILLMKSRNSCKDAEYGLYS 203
DB 108 FVYSQVVFSGKAYSPKATSSPLYLAEVQLFSSQYPPHVPILL-SSQKMWYVGLQEPWLHS 166

QY 204 IYGGIPELKENDRIFFSVVIN-EHLIDMDHEASFFGAF 240
DB 167 MYGGAARQLTQGDQLSTHTDGIPLHV-LSPSTVFFGAF 203

RESULT 9
QWMSN
N;Alternate names: cachectin; TNF alpha
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1988 #sequence, revision 31-Mar-1988 #text change 04-Feb-2000
C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696
R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Ito, H.
DNA 7, 193-201, 1988
A;Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis A;Reference number: A22908; MUID:88224564; PMID:2836146
A;Accession: A22908
A;Molecule type: DNA
A;Residues: 1-235 <SHI>
A;Cross-references: GB:M20155
R;Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl A;Reference number: S03791; MUID:87298639; PMID:3040015
A;Accession: S03791
A;Molecule type: DNA

A;Residues: 1-235 <SHA>
A;Cross-references: GB:M38296; NID:G202086; PIDN:AAA40459.1; PID:G202087
A;Note: article in Russian with English abstract
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor n A;Reference number: A93679; MUID:88067722; PMID:3684584
A;Accession: A27303
A;Molecule type: DNA
A;Residues: 1-235 <SEM>
A;Cross-references: GB:Y00467; NID:G54830; PIDN:CAA68530.1; PID:G54832
R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necro A;Reference number: A25164; MUID:85298296; PMID:3898078
A;Accession: A25164
A;Molecule type: mRNA
A;Residues: 1-235 <PEN>
A;Cross-references: GB:M11731; NID:G202084; PIDN:AAA40458.1; PID:G202085
R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, Nucleic Acids Res. 13, 4417-4429, 1985
A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic exp A;Reference number: A23127; MUID:85242112; PMID:2989794
A;Accession: A23127
A;Molecule type: mRNA
A;Residues: 1-235 <FRA>
A;Cross-references: GB:X02611; NID:G54844; PIDN:CAA26457.1; PID:G54845
R;Caeh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide result A;Reference number: A34251; MUID:89380231; PMID:2777790
A;Accession: A34251
A;Molecule type: protein
A;Residues: 70-87 <CSE>
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region (A;Reference number: I59058; MUID:86149365; PMID:2419912
A;Accession: I59058
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-230,'R',232-235 <RES>
A;Cross-references: GB:M13049; NID:G202082; PIDN:AAA40457.1; PID:G202083
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A;Title: Characterization of high molecular weight glycosylated forms of murine tumor I A;Reference number: A36696; MUID:91097531; PMID:2268312
A;Accession: A36696
A;Molecule type: protein
A;Residues: 80-85,'X',87-99 <SHE>
C;Genetics:
A;Introns: 62/3; 81/1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; men F;80-235/Product: tumor necrosis factor #status experimental <MAT>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

Query Match 9.48; Score 121; DB 1; Length 235;
Best Local Similarity 23.18; Pred. No. 0.0063;
Matches 43; Conservative 34; Mismatches 79; Indels 30; Gaps 8;
A;Accession: A27303; MUID:88067722; PMID:3684584

QY 67 EKOQNTSPLVREKGPORVAHITGTGRSNTLSSP-----NSKNEKALGRKINSWESSR 120
DB 62 EKFPNGPLI-----SSMAQTLLRSSSQSSDKPKVAHVVAHVHVEQL-----EMLSOR 111

QY 121 SGHSFSLNHLRNGELVHEKGFYIYKYSQYTFRRFQSEIKENTKNDKQMVQIYKYT-SYP 179
DB 112 ANALLGMDLKDNDQLVVPADGLVLYVQLFGQ-----GCPDYVLLTHTVTSRFAISYQ 166

QY 149 QTVFRFOEIKENTNDKQMVOYYTKYT-----SYDDPILLMKSARNCSWSK----DAE 198
Db ||| ||| :||| :
 98 QVLVR-----GHGCPSTPLFLTHISIAVSQTKNVLSAISKSPCHRETPEAK 148
 ||| |||| ||| :
QY 199 YGLYSIIQGIGFELKENDRIFSVVTNEHLIDMDHEAS-FFG 238
Db ||| |||| ||| :
 149 PWTEPIYGGVQLKEGRISAENIQPEYLDAESGGVVFG 189

RESULT 14

B27303
tumor necrosis factor beta precursor - mouse
N;Alternate names: lymphotoxin; TNF beta
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 24-Sep-1999
S;Accession: B27303; S01342; S10083; I56004; I48853; I55980
R;Samon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor ne-
crosis) gene.
A;Reference number: A93679; MUID:88067722; PMID:3684584
A;Accession: B27303
A:Molecule type: DNA
A;Residues: 1-202 <SB>
A;Cross-references: GB:X00467; NID:g54830; PIDN:CAG68529.1; PID:g54831
R:Nedospasov, S.A.; Hirt, B.; Shakhov, A.N.; Dobrynin, V.N.; Kawashima, E.; Accolla, R.,
Nucleic Acids Res. 14, 7713-7725, 1986
A;Title: The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) are
located at different positions on chromosome 6.
A;Reference number: S01342; MUID:87040736; PMID:3490653
A;Accession: S01342
A:Molecule type: DNA
A;Residues: 1-11,139-160,'CG',163-178 <NED>
A;Cross-references: EMBL:X06217
R;Weil, D.; Dutry, F.
Oncogene Res. 3, 409-414, 1988
A;Title: Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA i-
n rat fibroblasts by endotoxins or lipopolysaccharides.
A;Reference number: S10083; MUID:89144562; PMID:3147435
A;Accession: S10083
A:Molecule type: mRNA
A;Residues: 6-202 <WEI>
A;Cross-references: EMBL:X14800; NID:g54833; PIDN:CAA32906.1; PID:g736269
R;Garther, S.M.; Mock, B.A.; Hilgers, J.; Huppi, K.E.; Roeder, W.D.
J. Immunol. 139, 476-483, 1987
A;Title: Mouse lymphotoxin and tumor necrosis factor: Structural analysis of the cloned
genes.
A;Reference number: I56004; MUID:87252204; PMID:2885372
A;Accession: I56004
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-25,'P','27'-202 <RES>
A;Cross-references: GB:M17015; NID:g198880; PIDN:AAA39450.1; PID:g387407
R;Gray, P.W.; Chen, E.; Li, C.B.; Tang, W.L.; Ruddie, N.
Nucleic Acids Res. 15, 3937, 1987
A;Title: The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.
A;Reference number: I48853; MUID:87231097; PMID:3588316
A;Accession: I48853
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-202 <RE2>
A;Cross-references: EMBL:Y00137; NID:g54842; PIDN:CAA68330.1; PID:g54843
R;Li, C.

J. Immunol. 138, 4496-4501, 1987
A;Title: Cloning and expression of murine lymphotoxin cDNA.
A;Reference number: I55980; MUID:87224127; PMID:2884262
A;Accession: I55980
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-202 <RE3>
A;Cross-references: GB:M16819; NID:g202088; PIDN:AAA40460.1; PID:g202089
C;Comment: The first intron occurs in the 5' untranslated region.
C;Genetics:
A;Gene: Tnf
A;Map position: 17
A;Introns: 32/3; 66/1

C;Superfamily: tumor necrosis factor

C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

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Query Match      8.9%; Score 114; DB 1; Length 202;
Best Local Similarity 23.5%; Pred. No. 0.02;
Matches 38; Conservative 25; Mismatches 81; Indels 18; Gaps 3;

QY 80 GPORVAHITGTRGNTLSSPNSKNEKALGRKINWESSRSGHSFLSNHLRNGELVIH 139
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 GILKPAHLVGYESKNSL-----LWRASDRAFLRHGFSLSNNSLLIP 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 140 EKGFIYISQTYRFRFOEIKENTKNDKQMVQYIYKYTS-YPDPILLMKSGARNSCKDAE 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 100 TSGLYFYVQWVPSGSCSPRAIPTPIYLAHEVQLFSSQYPPFVPLL-SAQKSVYPLQG 158
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 199 YGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 159 PWVRSMYQGAFLLSKGDQLSTHTDGTGISHLHFSFSSVFFGAF 200
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 15

S52715

tumor necrosis factor alpha precursor - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000

C;Accession: S52715

R;Mertens, B.; Gaidulis, L.

submitted to the EMBL Data Library, March 1995

A;Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and bo

A;Reference number: S52715

A;Accession: S52715

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-185 <MER>

A;Cross-references: EMBL:Z48808; NID:g755701; PIDN:CAA88743.1; PID:g755702

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein

F;33/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;97-129/Disulfide bonds: #status predicted

```
Query Match      8.8%; Score 113.5; DB 2; Length 185;
Best Local Similarity 25.0%; Pred. No. 0.02;
Matches 45; Conservative 29; Mismatches 79; Indels 27; Gaps 9;

QY 80 GPORVAHITGTRGRS---NTL-SSPNSKNEKALGR---KINS-----WESSRSGHSFLS 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 GPQREESPGGPSINSLVTLRSSQASSNKKPVAVHVVDINSPGQURWWDSYANALMAN 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 NLHLRNGELVIHEKGFYIYISQTYRFRQEEIKENTKNDKQMVQYIYK--YTSYPDPILLM 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 GVKLEDNQLVVPADGLYLIYSQVLFRCQ----GCPSTPLFLTHTISRIAVSYQTKVNIL 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 KSAARNSC-----WSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 SATKSPCHRETPWA-BAKPWYEPYQGGVQLEKGDRLSAEINLPDYLDYAESGGQYVFG 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Search completed: March 23, 2004, 09:15:49

Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:07:59 ; Search time 17 Seconds
(without alignments)

744.297 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287
Sequence: 1 TNELKOMQDKYKSGIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 56376

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160	12.4	174	1 TN15 HUMAN	O95150 homo sapien
2	159.5	12.4	240	1 TN14 HUMAN	O43557 homo sapien
3	152.5	11.8	239	1 TN14 MOUSE	Q9qy99 mus musculus
4	136.5	10.6	235	1 TNFA RABIT	P04924 oryctolagus
5	134.5	10.5	204	1 TNFB PIG	P26445 sus scrofa
6	132.5	10.3	234	1 TNFA CAVPO	P51435 cavia porce
7	130	10.1	232	1 TNFA PIG	P23563 sus scrofa
8	129.5	10.1	235	1 TNFA PERLE	P36939 peromyscus
9	127.5	9.9	234	1 TNFB BOVIN	Q06600 bos taurus
10	126	9.8	234	1 TNFA HORSE	P29553 equus caball
11	125	9.7	233	1 TNFA MARMO	O35734 marmota mon
12	123	9.6	233	1 TNFA HUMAN	P01375 homo sapien
13	122.5	9.5	229	1 TNFA CEREL	P51743 cervus elap
14	122	9.5	205	1 TNFB HUMAN	P01374 homo sapien
15	122	9.5	232	1 TNFA PANTR	Q8hzd9 pan troglod
16	121	9.4	235	1 TNFA MOUSE	P06804 mus musculus
17	121	9.4	235	1 TNFA RAT	P16599 rattus norv
18	120	9.3	205	1 TNFB MARMO	Q9jmb9 marmota mon
19	120	9.3	233	1 TNFA PAPSP	P33620 papio sp. (
20	118	9.2	233	1 TNFA TURTR	Q9bea1 turisiops tr
21	117.5	9.1	201	1 TNFA MACEU	Q9xt48 macropus eu
22	117.5	9.1	234	1 TNFA SHEEP	P23383 ovis aries
23	117	9.1	233	1 TNFA MACMU	P48094 macaca mula
24	117	9.1	233	1 TNFA PAPHU	O77510 papio hamad
25	116.5	9.1	233	1 TNFA CANFA	P51742 canis fami
26	116	9.0	233	1 TNFA MACFA	P79337 macaca fasc
27	116	9.0	233	1 TNFA SAISC	Q8mkc8 saimiri sci
28	114	8.9	202	1 TNFB MOUSE	P79235 mus musculus
29	113.5	8.8	233	1 TNFA TRIVU	P09374 trichosurus
30	113.5	8.8	234	1 TNFA BOSIN	P59684 bos indicus
31	113	8.8	233	1 TNFA BOVIN	Q06599 bos taurus
32	113	8.8	233	1 TNFA BURBU	P59693 bubalus bub
33	113	8.8	233	1 TNFA_LANGL	P59694 lama glama

RESULT 1

ID	TN15_HUMAN	STANDARD;	PRT;	174 AA.
AC	O95150;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	tumor necrosis factor ligand superfamily member 15 (Vascular endothelial cell growth inhibitor) (TNF ligand-related molecule 1).			
GN	TNFSF15 OR VEGI OR TLI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Umbilical vein;			
RX	MEDLINE=99091541; PubMed=9872942;			
RA	Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,			
RA	Janat F., Kozak D., Xu S., Rojase L., Aggarwal B.B., Ruben S.,			
RA	Li L.-Y., Gentz R., Yu G.-L.;			
RT	"VEGI", a novel cytokine of the tumor necrosis factor family, is an angiogenesis inhibitor that suppresses the growth of colon carcinomas in vivo."			
RL	FASEB J. 13:181-189(1999).			
CC	-!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis (in vitro).			
CC	-!- SUBUNIT: Homotrimer (Potential).			
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).			
CC	-!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells. Detected in placenta, lung, kidney, skeletal muscle, pancreas, spleen, prostate, small intestine and colon.			
CC	-!- SIMILARITY: Belongs to the tumor necrosis factor family.			
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CC	EMBL; AF039390; RAD08783.1; -			
DR	HSSP; P50591; IDOG.			
DR	Genew; HGNC:11931; TNFSF15.			
DR	MIM; 604052; -			
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.			
DR	GO; GO:0005102; F:receptor binding; TAS.			
DR	GO; GO:0000074; P:regulation of cell cycle; TAS.			
DR	GO; GO:0000074; P:regulation of cell cycle; TAS.			
DR	InterPro; IPR006053; TNF_ab.			
DR	InterPro; IPR006052; TNF_family.			
DR	InterPro; IPR008983; TNF_like.			
DR	InterPro; IPR003636; TNF_subf.			
DR	Pfam; PF00229; TNF_1.			
DR	PRINTS; PR01234; TNECROSISFCT.			
DR	ProDom; PD002012; TNF_subf; 1.			

ALIGNMENTS

ID	TN15_HUMAN	STANDARD;	PRT;	174 AA.
AC	O95150;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	tumor necrosis factor ligand superfamily member 15 (Vascular endothelial cell growth inhibitor) (TNF ligand-related molecule 1).			
GN	TNFSF15 OR VEGI OR TLI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Umbilical vein;			
RX	MEDLINE=99091541; PubMed=9872942;			
RA	Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,			
RA	Janat F., Kozak D., Xu S., Rojase L., Aggarwal B.B., Ruben S.,			
RA	Li L.-Y., Gentz R., Yu G.-L.;			
RT	"VEGI", a novel cytokine of the tumor necrosis factor family, is an angiogenesis inhibitor that suppresses the growth of colon carcinomas in vivo."			
RL	FASEB J. 13:181-189(1999).			
CC	-!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis (in vitro).			
CC	-!- SUBUNIT: Homotrimer (Potential).			
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).			
CC	-!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells. Detected in placenta, lung, kidney, skeletal muscle, pancreas, spleen, prostate, small intestine and colon.			
CC	-!- SIMILARITY: Belongs to the tumor necrosis factor family.			
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CC	EMBL; AF039390; RAD08783.1; -			
DR	HSSP; P50591; IDOG.			
DR	Genew; HGNC:11931; TNFSF15.			
DR	MIM; 604052; -			
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.			
DR	GO; GO:0005102; F:receptor binding; TAS.			
DR	GO; GO:0000074; P:regulation of cell cycle; TAS.			
DR	GO; GO:0000074; P:regulation of cell cycle; TAS.			
DR	InterPro; IPR006053; TNF_ab.			
DR	InterPro; IPR006052; TNF_family.			
DR	InterPro; IPR008983; TNF_like.			
DR	InterPro; IPR003636; TNF_subf.			
DR	Pfam; PF00229; TNF_1.			
DR	PRINTS; PR01234; TNECROSISFCT.			
DR	ProDom; PD002012; TNF_subf; 1.			

```

DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT 26 174 EXTRACELLULAR (POTENTIAL).
FT 85 125 POTENTIAL.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 174 AA; 20131 MW; CCB83BA7EE673B98 CRC64;

Query Match 12.4%; Score 160; DB 1; Length 174;
Best Local Similarity 35.3%; Pred. No. 2.5e-06;
Matches 49; Conservative 24; Mismatches 48; Indels 18; Gaps 8;

QY 116 WESSRSGHSLN-LHLRNGELVTHEKGFYIYSQTYFRFQ-----EIKENTKDK-QM 168
Db 42 WE-HELGLATKRMVNTNFKLLIPESGDYFIYSQTYFRGWTSECSIRAGRNKPDISI 100

QY 169 VQIYKYT-SYDPILLMKARNSCWSKDAEYG---LYSYQGIFFELKENDRIFVSVTN 224
Db 101 TVVITKVTDSYPETQLMGTSVC-----EVGSNWFQPIYLGAMFSLQEGDKLMNVNSD 155

QY 225 EHLIDMDHE-ASRFGAEIV 242
Db 156 ISLVDTYTKDKTFPGAELL 174

RESULT 2
ID _TN14_HUMAN STANDARD; Q8WVF8; PRT; 240 AA.
AC O43557; O75476; Q8WVF8; Q96L22;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
DE mediator-ligand) (HVEM-L).
GN TNFSF14 OR LIGHT OR HVEML.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98122340; PubMed=9462508;
RA Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
RA Ware C.F.;
RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
RT ligands for herpesvirus entry mediator."
RL Immunity 8:21-30(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Liver;
RX MEDLINE=98438532; PubMed=9765287;
RA Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
RA Tan K.B., Dede K., Spanpanato J., Silverman C., Hensley P.,
RA DiPrinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
RA Truneh A., Young P.R.;
RT "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
RT HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell
RT growth."
RL J. Biol. Chem. 273:27548-27556(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
RX MEDLINE=21528948; PubMed=11673523;
RA Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
RT "Genomic characterization of LIGHT reveals linkage to an immune
RT response locus on chromosome 19p13.3 and distinct isoforms generated
RT by alternate splicing or proteolysis."
RL J. Immunol. 167:5122-5128(2001).
RN [4]

SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
CC decoy receptor TNFRSF6B modulates its effects. Activates NFkB,
CC stimulates the proliferation of T cells, and inhibits growth of
CC the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex
CC virus.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC (isoform 1); Cytoplasmic (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O43557-1; Sequence=Displayed;
CC Name=2; Synonyms=LIGHT delta-TM;
CC IsoId=O43557-2; Sequence=VSP_006452;
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
CC FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
CC TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
CC AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
CC NONHEMATOPOIETIC TUMOR LINES.
CC -!- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
CC -!- PTM: N-glycosylated.
CC -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC by proteolytic processing.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 178.
CC -----
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CC -----
CC EMBL; AF036581; AAC39563.1; -
CC EMBL; AF064090; AAC25169.1; -
CC EMBL; AY028261; AAK26160.1; -
CC EMBL; BC018058; AAH18058.1; ALT_FRAME.
CC HSSP; P01375; 4TSV.
CC Genew; HGNC:11930; TNFSF14.
CC MIM; 604520; -
CC GO; GO:005102; F:receptor binding; TAS.
CC GO; GO:0006917; P:induction of apoptosis; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR006053; TNF_ab.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.

```


TNFA_RABBIT
ID TNFA_RABBIT STANDARD; PRT; 235 AA.
AC P04924;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9106534; PubMed=2249779;
RA Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
RA Nedopasov S.A.;
RT "Structural analysis of the rabbit TNF locus, containing the genes
RT encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
RT factor).";
RL Gene 95:215-221(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86219712; PubMed=3519138;
RA Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W.,
RA Wallace R.B.;
RT "Molecular cloning of the gene encoding rabbit tumor necrosis
RT factor.";
RL DNA 5:157-165(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86219711; PubMed=3519137;
RA Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,
RA Hayashi H., Kato M., Seko M.;
RT "Molecular cloning and expression in Escherichia coli of the cDNA
RT coding for rabbit tumor necrosis factor.";
RL DNA 5:143-155(1986).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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CC or send an email to license@isb-sib.ch).

CC EMBL; M12845; AAA31486.1; -
CC EMBL; M12846; AAA31482.1; -
CC EMBL; M60340; AAA31484.1; -
CC PIR; A25454; A25451.
CC HSSP; P06804; 2TNF.
CC InterPro; IPR006053; TNF_abc.

DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 235 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 80 235 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 57 235 EXTRACELLULAR (POTENTIAL).
FT SITE 79 90 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CKL) (BY SIMILARITY).
FT DISULFID 148 179 BY SIMILARITY.
FT CONFLICT 63 63 MISSING (IN REF. 3).
SQ SEQUENCE 235 AA; 25816 MW; 610177D0BD2EF871 CRC64;
Query Match 10.6%; Score 136.5; DB 1; Length 235;
Best Local Similarity 23.0%; Pred. No. 0.00032;
Matches 42; Conservative 37; Mismatches 81; Indels 23; Gaps 7;
QY 72 IGPLVERGQRVAAHITCTGRSNTL-SPNSKNEKALGRKINS-----WESSRSQ 122
Db 56 IGQEEEQSPNNL--HLVNPVAVMTLRASRALSCKPLAHVVANPQVEGQLQWLSQAN 113
QY 123 HSFLSNLHRLNGELVHEKGFYIYSQTYFRQBEIKENTKNDKQWQVIYKY-TSYDDP 181
Db 114 ALLANGMKLTQNLVVPADGLYIYSQVLFSGQ-----GCRSYVLLTHTVSFAVSYPNK 168
QY 182 IILMKARNSCWSKDAEYG----LYSIYOGGFFELKENDRIFVSVTNEHLIDMDHEAS- 235
Db 169 VNLISAKSPCHRETPPEAEPMWVPIYLGQVQLEKGDRLSTEVNQPEYLDLAESQGV 228
QY 236 FFG 238
Db 229 YFG 231
RESULT 5
TNFB_PIG STANDARD; PRT; 204 AA.
ID TNFB_PIG
AC P26445;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE factor ligand superfamily member 1).
GN LTA OR TNFSF1 OR TNFB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91340150; PubMed=1874444;
RA Kuhnert P., Wuthrich C., Peterhans E., Pauli U.;
RT "The porcine tumor necrosis factor-encoding genes: sequence and
RT comparative analysis.";
RL Gene 102:171-178(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Fibroblast;
RX MEDLINE=21108615; PubMed=11169259;
RA Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
RA Renard C.;
RT "Sequence of the swine major histocompatibility complex region
RT containing all non-classical class I genes.";

```

RL Tissue Antigens 57:55-65(2001).
CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its
CC heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC produced by lymphocytes and cytotoxic for a wide range of tumor
CC cells in vitro and in vivo.
CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC associated (heterotrimers) (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC EMBL; X54859; CAA38638.1; -.
CC EMBL; AJ251914; CAB63853.1; -.
CC PIR; S17289; S17289.
CC HSSP; P01374; 1TNR.
CC InterPro; IPR006053; TNF abc.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS50049; TNF 2; 1.
CC Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 33
FT CHAIN 34 204 LYMPHOTOXIN-ALPHA.
FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 204 AA; 21960 MW; 81263187435E56AC CRC64;

Query Match
Best Local Similarity 10.5%; Score 134.5; DB 1; Length 204;
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;

QY 63 STVQEQQNISPLVRGPGFQVAHITG-----TGRSNTLSSPNSKNEKALGRKINS 115
Dd 42 SAAQPAHQH-PPKHLARGTLKPAHLVGDPTDPSLRWRANT-----DRAFLA---- 88

QY 116 WESSRSGHSLNLHLRNGELVIEHKGYIYISQTYFRQEEIKENTKDKOMQVVIYKY 175
Dd 89 -----HGFL-----LSNNSLAVPTSGLVFVYSQVVFSGCGCPKATPTPLVLAHEVQVF 137

QY 176 TS-YDPFILLMKSARNSCWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEA 234
Dd 138 SSQYPPHVLSSAKQSCVCPQCPWP-VRSVYQGVAVFLIQDQLSTHTDGTTHLLSPSS 196

QY 235 SFFGAF 240
Dd 197 VFFGAF 202

RESULT 6
TNFA_CAVPO STANDARD; PRT; 234 AA.
AC P51435;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
GN TNF OR TNFSF2 OR TNFA.
OS Cavia porcellus (Guinea pig).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]_TaxID=10141;
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Lung;
RA Yuan H.T., Kelly F.J., Bingle C.D.;
RT "Cloning and characterisation of guinea pig TNF-alpha cDNA.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Dunkin-Hartley;
RA MEDLINE=97462215; PubMed=9316485;
RX White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT factor-alpha.";
RL Am. J. Physiol. 273:L524-L530(1997).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U39839; AAB06492.1; -.
CC EMBL; U77036; AAB19210.1; -.
CC HSSP; P06804; 2TNF.
CC InterPro; IPR006053; TNF abc.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS50049; TNF 2; 1.
CC Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
KW TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 1 234 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 80 234 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).
FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 147 178 BY SIMILARITY.
SQ SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match
Best Local Similarity 10.3%; Score 132.5; DB 1; Length 234;
Best Local Similarity 24.6%; Pred. No. 0.00068;

```

Matches	44; Conservative	33; Mismatches	77; Indels	25; Gaps	7;
QY	80	GPORVAAHITGT--RGRSNTL----	SSPNSKNEKALGRKINS-----	WESSRSGHSFL	126
				:	:
				:	:
				:	:
Db	57	GPQREEQFGSPFRPLAQTLTLRSASQNDNDKPAHVANQAQEELQWLSKEANALLA	116		
				:	:
				:	:
				:	:
QY	127	SNHLRNGELVIEHKGYPIYYISQYTFRQBEIKENTKNDKQMOYIYKY-TSYDPDILLM	185		
				:	:
				:	:
Db	117	NGMGLSDNQLWPSDGLYIYSQVLFKQ-----	GCPSYLLLTHTVSRKLAVSYPEKVNLL	171	
				:	:
				:	:
QY	186	KSARNCSWKDAEYG-----	LYSIYQGIPELKENDRIFVSVTNEHLIDM-DHEASFFG	238	
				:	:
				:	:
				:	:
Db	172	SAIKSPCKQETPEGAERKPMYETILGVFQLOKQDRLSAEVNLPQVLDADSGQIYFG	230		
				:	:
				:	:
				:	:

RESULT 7	TFNA_PIG	TFNA_PIG	STANDARD;	PRT;	232 AA.
AC	P23563;				
DT	01-NOV-1991	(Rel. 20, Created)			
DT	01-NOV-1991	(Rel. 20, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (TNF-a) (Cachectin).				
DE	TNF OR TNFSF2 OR TNFA.				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9823;				
LN	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=91016861;	PubMed=2216741;			
RA	Drews R.T., Coffee B.W., Prastwood A.K., McGraw R.A.;				
RA	"Gene sequence of porcine tumor necrosis factor alpha.";				
RL	Nucleic Acids Res. 18:5564-5564 (1990).				
LN	[2]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=liver;				
RC	MEDLINE=91340150;	PubMed=1874444;			
RA	Kuhnert P., Wuehrich C., Peterhans E., Pauli U.;				
RA	"The porcine tumor necrosis factor-encoding genes: sequence and comparative analysis.";				
RL	Gene 102:171-178 (1991).				
LN	[3]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=Macrophage;				
RC	Choi C.S., Mollitor T.W., Lin G.F., Murtaugh M.P.;				
RA	"Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis factor-alpha.";				
RL	Anim. Biotechnol. 2:97-105 (1991).				
LN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=large white;	TISSUE=Fibroblast;			
RX	MEDLINE=21108615;	PubMed=11169259;			
RA	Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M., Renard C.;				
RA	"Sequence of the swine major histocompatibility complex region containing all non-classical class I genes.";				
RL	Tissue Antigens 57:55-65 (2001).				
LN	[5]				
RP	SEQUENCE OF 44-232 FROM N.A.				
RP	MEDLINE=90034181;	PubMed=2478420;			
RA	Pauli U., Beutler B., Peterhans E.;				
RA	"Porcine tumor necrosis factor alpha: cloning with the polymerase chain reaction and determination of the nucleotide sequence.";				
RL	Gene 81:185-191 (1989).				
CC	-1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFRSF1B/TNFR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia. Under certain conditions it can stimulate cell proliferation and induce cell differentiation.				

DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 DE ligand superfamily member 2) (TNF-a) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Peromyscus leucopus (White-footed mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Peromyscus.
 OX NCBI_TaxID=10041;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92218012; PubMed=1348497;
 RA Crew M.D., Filipowski M.E.;
 RT "Sequence of the tumor necrosis factor/cachectin (TNF) gene from
 RT Peromyscus leucopus (family Cricetidae).";
 RL Immunogenetics 35:351-353(1992).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
 CC cancer and infection, and is characterized by general ill health
 CC and malnutrition.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M59233; AAA40596.1; -;
 CC F1R; I54490; I54490.
 CC HSP; P06804; 2TNF.
 CC InterPro; IPR006053; TNF_abc.
 CC InterPro; IPR006052; TNF_family.
 CC InterPro; IPR008983; TNF_like.
 CC Pfam; PF00229; TNF; 1.
 CC PRINTS; PR01234; TNCRSISFCT.
 CC ProDom; PD002012; TNF_subf; 1.
 CC SMART; SM00207; TNF; 1.
 CC PROSITE; PS00251; TNF_1; 1.
 CC PROSITE; PS0049; TNF_2; 1.
 CC Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
 FT CHAIN 1 235 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT CHAIN 80 235 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 57 235 EXTRACELLULAR (POTENTIAL).
 FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 FT DISULFID 148 179 BY SIMILARITY.
 FT CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 235 AA; 25822 MW; 235A5CFC9F9AC624 CRC64;

Query Match 10.1%; Score 129.5; DB 1; Length 235;

Best Local Similarity 24.5%; Pred. No. 0.0012;
 Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;
 QY 72 ISPLVREGRGQVAAHITGRGSRNTL-SSPNSKNEKALGRKINSWE-----SRSCH 123
 DB 56 IGQREKEFPNNLP--IGSMAQTLLRSSSQSSDKPAHVAVVANHVDQLEWLGRGAN 113
 QY 124 SFLSN-LHLRNGELVTHKGFVYISQTYFRFOEIKENTKNDKQMVQYIKY-TSYDPD 181
 DB 114 ALLANGMDLKDNLVTPADGLVIVSQVLFKG-----GCSSVVLTHVSRFAVSIEDK 168
 QY 182 IILMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
 DB 169 VALLSAIKSPC-PKETPEGSELKPWEPIYLGGVFQLEKGRDLRAEVLNPKYLDFAESGQ 227
 QY 236 -PFG 238
 DB 228 VYFG 231
 RESULT 9
 ID TNFB_BOVIN STANDARD; PRT; 204 AA.
 AC Q06600;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lymphotoxin-alpha precursor (Lr-alpha) (TNF-beta) (Tumor necrosis
 DE factor ligand superfamily member 1).
 GN LTA OR TNFSF1 OR TNFB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94083525; PubMed=8260599;
 RA Cludts I., Cleuter Y., Kettmann R., Burny A., Droogmans L.;
 RT "Cloning and characterization of the tandemly arranged bovine
 RT lymphotoxin and tumour necrosis factor-alpha genes.";
 RL Cytokine 5:336-341(1993).
 CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to
 CC TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its
 CC heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
 CC produced by lymphocytes and cytotoxic for a wide range of tumor
 CC cells in vitro and in vivo.
 CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
 CC LTA subunits or (less prevalent) two LTA and one LTB subunits (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
 CC associated (heterotrimers) (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Z14137; CAA78510.1; -;
 CC F1R; I46046; S24641.
 CC HSP; P01374; 1TNB.
 CC InterPro; IPR006053; TNF_abc.
 CC InterPro; IPR006052; TNF_family.
 CC InterPro; IPR008983; TNF_like.
 CC InterPro; IPR003636; TNF_subf.
 CC Pfam; PF00229; TNF; 1.
 CC PRINTS; PR01234; TNCRSISFCT.
 CC ProDom; PD002012; TNF_subf; 1.
 CC SMART; SM00207; TNF; 1.

KW	Cytokine; Transmembrane; Signal; Anchoring; Phosphorylation.
FT	CHAIN 1 233
FT	CHAIN 78 233
FT	DOMAIN 1 35
FT	TRANSMEM 36 56
FT	DOMAIN 57 233
FT	SITE 77 78
FT	MOD RES 2 2
FT	DISULFID 146 177
SQ	SEQUENCE 233 AA; 25764 MW; 34D3D1965DAAE0E7 CRC64;

Query Match 9.7%; Score 125; DB 1; Length 233;
 Best Local Similarity 23.2%; Pred. No. 0.0028;
 Matches 36; Conservative 30; Mismatches 69; Indels 20; Gaps 5;

QY	99	SSPNSKNEKALGRKINS-----WESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQT	150
DB	80	SSSQNWMDKPVAVHVAKNDEKQELWLSRRANALLANGMELINQLVVPANGLYLVYSQV	133
QY	151	YFRFQBEIKENTKNDKQMVQYIKY-TSYPDPTILLMKSAENSQWCKDAEYGLYS-----I	204
DB	140	LFKQG-----GCFPSYLLTHTVSFPAVSQDKYNLLSAIKSPCKESLGAEFPKWPEPI	194
QY	205	YQGGIFELKENDRIFSVTVNEHLIDMDHEAS-FFG	238
DB	195	YLGVPFELQKGDRLSAEVLNLPYSLDFAESGQVYFG	229

RESULT 12

TNFA_HUMAN					
ID	TNFA_HUMAN	STANDARD;	PRT;	233	AA.
AC	P01375; O43647; Q9P1Q2; Q9UIV3;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor				
DE	ligand superfamily member 2) (TNF-a) (Cachectin).				
GN	TNF OR TNFSP2 OR TNFA.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID:9606;				
RX	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=87217060; PubMed=3555974;				
RA	Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,				
RA	Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,				
RA	Filippov S.A., Bystrov N.S., Boldyreva B.F., Chuvpilo S.A.,				
RA	Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;				
RT	"Random arrangement of genes coding for tumor necrosis factor (TNF-				
RT	alpha) and lymphotoxin (TNF-beta) in the human genome.";				
RL	Cold Spring Harb. Symp. Quant. Biol. 51:611-624 (1986).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=85086244; PubMed=6329892;				
RA	Pennica D., Nedwin G.E., Hayflick J.S., Seeburg P.H., Derynck R.,				
RA	Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.;				
RT	"Human tumour necrosis factor: precursor structure, expression and				
RT	homology to lymphotoxin.";				
RL	Nature 312:724-729 (1984).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=85137898; PubMed=3883195;				
RA	Shirai T., Yanaguchi H., Ito H., Todd C.W., Wallace R.B.;				
RT	"Cloning and expression in Escherichia coli of the gene for human				
RT	tumour necrosis factor.";				
RL	Nature 313:803-806 (1985).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=86016093; PubMed=2995927;				
RA	Nedwin G.E., Taylor S.L., Sakaguchi A.Y., Smith D.H.,				
RA	Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;				

RT "Human lymphotoxin and tumor necrosis factor genes: structure,
 RT homology and chromosomal localization.";
 RL Nucleic Acids Res. 13:6361-6373(1985).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85142190; PubMed=3856324;
 RA Wang A.M., Creasey A.A., Ladner M.B., Lin L.S., Strickler J.,
 RA Wardsell J.N., Yamamoto R., Mark D.F.;
 RA "Molecular cloning of the complementary DNA for human tumor necrosis
 RT factor.";
 RL Science 228:149-154(1985).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86030296; PubMed=3932069;
 RA Marmenout A., Fransen L., Tavernier J., van der Heyden J., Tizard R.,
 RA Kawashima E., Shaw A., Johnson M.J., Semon D., Mueller R.,
 RA Ruysschaert M.R., van Vliet A., Fiers W.;
 RA "Molecular cloning and expression of human tumor necrosis factor and
 RT comparison with mouse tumor necrosis factor.";
 RL Eur. J. Biochem. 152:515-522(1985).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9327029; PubMed=8499947;
 RA Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
 RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
 RA Cohen D.;
 RA "Dense Ali clustering and a potential new member of the NF kappa B
 RT family within a 90 kilobase HLA class III segment.";
 RL Nat. Genet. 3:137-145(1993).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9327029; PubMed=8499947;
 RA Neville M.J., Milner C.M., Campbell R.D.;
 RA "A new member of the immunoglobulin superfamily and a V-ATPase G
 RT subunit are amongst the predicted products of novel genes close to the
 RT TNF locus in the human MHC.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91184128; PubMed=2009860;
 RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
 RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
 RA Lasky S., Hood L.;
 RA "Sequence of the human major histocompatibility complex class III
 RT region.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93018820; PubMed=1402651;
 RA Shima S., Tamiya G., Oka A., Inoko H.;
 RA "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93018820; PubMed=1402651;
 RA Shima T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.;
 RA "Genome diversity in HLA: a new strategy for detection of genetic
 RT polymorphisms in expressed genes within the HLA class III and class I
 RT regions.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93018820; PubMed=1402651;
 RA Rieder M.J., Carrington D.P., Lee K.L., Livingston R.J., Daniels M.R.,
 RA Montoya M.A., Chung M.-W., Yi Q., Miyamoto K.E., Nguyen C.P.,
 RA Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
 RA Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93018820; PubMed=1402651;
 RA Shima S., Tamiya G., Oka A., Inoko H.;
 RA "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP SEQUENCE OF 77-233 FROM N.A.
 RX MEDLINE=93018820; PubMed=1402651;
 RA Jang J.S., Kim B.E.;
 RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [15]
 RP SEQUENCE OF 84-214 FROM N.A.
 RX MEDLINE=93018820; PubMed=1402651;
 RA Shao C., Yan W., Zhu F., Yue W., Chai Y., Zhao Z., Wang C.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP PHOSPHORYLATION (MEMBRANE FORM).
 RX MEDLINE=96170872; PubMed=8597870;
 RA Pocsik E., Duda E., Wallach D.;
 RA "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in
 RT transfected HeLa cells.";
 RL J. Inflamm. 45:152-160(1995).
 RN [17]
 RP PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.
 RX MEDLINE=99221647; PubMed=10205166;
 RA Watts A.D., Hunt N.H., Wanigasekara Y., Bloomfield G., Wallach D.,
 RA Roufogalis B.D., Chaudhri G.;
 RA "A casein kinase I motif present in the cytoplasmic domain of members
 RT of the tumor necrosis factor ligand family is implicated in 'reverse
 RL signalling'.";
 RN EMBO J. 18:2119-2126(1999).
 RP MUTAGENESIS.
 RX MEDLINE=91184128; PubMed=2009860;
 RA Ostade X.V., Tavernier J., Prange T., Fiers W.;
 RA "Localization of the active site of human tumor necrosis factor
 RT (hTNF) by mutational analysis.";
 RL EMBO J. 10:827-836(1991).
 RN [19]
 RP MYRISTOYLATION.
 RX MEDLINE=93018820; PubMed=1402651;
 RA Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.;
 RA "Myristyl acylation of the tumor necrosis factor alpha precursor on
 RT specific lysine residues.";
 RL J. Exp. Med. 176:1053-1062(1992).
 RN [20]
 RP CLEARANCE BY ADAM17.
 RX MEDLINE=97186575; PubMed=9034191;
 RA Moes M.L., Jin S.-L.C., Milla M.E., Burkhardt W., Carter H.L.,
 RA Chen W.-J., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,
 RA Kost T.A., Lambert M.H., Leesnitzer M.A., McCauley P., McGeehan G.,
 RA Mitchell J., Moyer M., Pahel G., Rocque W., Overton L.K., Schoenen F.,
 RA Seaton T., Su J.-L., Warner J., Willard D., Becherer J.D.;
 RA "Cloning of a disintegrin metalloproteinase that processes precursor
 RT tumour-necrosis factor-alpha.";
 RL Nature 385:733-736(1997).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=89159409; PubMed=2922050;
 RA Jones E.Y., Stuart D.I., Walker N.P.;
 RA "Structure of tumor necrosis factor.";
 RL Nature 338:225-228(1989).
 RN [22]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=91193276; PubMed=1964681;
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RT alpha) and lymphotoxin (TNF-beta) in the human genome.";
RL Cold Spring Harb. Symp. Quant. Biol. 51:611-624 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86086150; PubMed=30011109;
RA Nedwin G.E., Jarrett-Nedwin J., Smith D.H., Naylor S.L.,
RA Sakaguchi A.Y., Goeddel D.V., Gray P.W.;
RT "Structure and chromosomal localization of the human lymphotoxin
RT gene.";
RL J. Cell. Biochem. 29:171-181 (1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87057135; PubMed=3536896;
RA Kobayashi Y., Miyamoto D., Asada M., Obinata M., Osawa T.;
RT "Cloning and expression of human lymphotoxin mRNA derived from a
RT human T cell hybridoma.";
RL J. Biochem. 100:727-733 (1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=85086243; PubMed=6334807;
RA Gray P.W., Agarwal B.B., Benton C.V., Bringham T.S., Henzel W.J.,
RA Jarrett J.A., Leung D.W., Moffat B., Ng P., Svedersky L.P.,
RA Palladino M.A., Nedwin G.E.;
RT "Cloning and expression of cDNA for human lymphotoxin, a lymphokine
RT with tumour necrosis activity.";
RL Nature 312:721-724 (1984).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=92339500; PubMed=1353024;
RA Matsuyama N., Okawa N., Tsukii Y., Endo T., Kaji A.;
RT "Nucleotide sequence of a cDNA encoding human tumor necrosis factor
RT beta from B lymphoblastoid cell RPMI 1788.";
RL FEBS Lett. 302:141-144 (1992).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=93372029; PubMed=8499947;
RA Iris F.J.M., Bouguetel L., Prieur S., Caterina D., Primas G.,
RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
RA Cohen D.;
RT "Dense Alu clustering and a potential new member of the NF kappa B
RT family within a 90 kilobase HLA class III segment.";
RL Nat. Genet. 3:137-145 (1993).
RN [7]
RP SEQUENCE FROM N.A.
RA Neville M.J., Milner C.M., Campbell R.D.;
RT "A new member of the immunoglobulin superfamily and a V-ATPase G
RT subunit are amongst the predicted products of novel genes close to the
RT TNF locus in the human MHC.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Shiina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
RA Lasky S., Hood L.;
RT "Sequence of the human major histocompatibility complex class III
RT region.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A., AND VARIANTS ARG-13; PRO-51 AND ASN-60.
RA Rieder M.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [11]
RP PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND VARIANT ASN-60.
RX MEDLINE=93083656; PubMed=1451807;
RA Voigt C.G., Maurer-Fogy I., Adolf G.R.;
RT "Natural human tumor necrosis factor beta (lymphotoxin). Variable O-
RT glycosylation at thr7, proteolytic processing, and allelic

variation.";
RL FEBS Lett. 314:85-88 (1992).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=92129275; PubMed=1733919;
RA Eck M.J., Ultsch M., Rinderknecht E., de Vos A.M., Sprang S.R.;
RT "The structure of human lymphotoxin (tumor necrosis factor-beta) at
RT 1.9-A resolution.";
RL J. Biol. Chem. 267:2119-2122 (1992).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 61-205 OF COMPLEX WITH
RP TNFR1.
RX MEDLINE=93258809; PubMed=8387891;
RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,
RA Broger C., Loetscher H., Lesslauer W.;
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT beta complex: implications for TNF receptor activation.";
RL Cell 73:431-445 (1993).
RN [14]
RP VARIANT ASN-60.
RX MEDLINE=91086846; PubMed=1670638;
RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,
RA Riethmuller G., Weiss E.H.;
RT "Polymorphic structure of the tumor necrosis factor (TNF) locus: an
RT NcoI polymorphism in the first intron of the human TNF-beta gene
RT correlates with a variant amino acid in position 26 and a reduced
RT level of TNF-beta production.";
RL J. Exp. Med. 173:209-219 (1991).
RN [15]
RP VARIANT PRO-125.
RX MEDLINE=91139175; PubMed=1671667;
RA Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;
RT "Haplotypic polymorphisms of the TNF gene.";
RL Immunogenetics 33:50-53 (1991).
CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its
CC heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC produced by lymphocytes and cytotoxic for a wide range of tumor
CC cells in vitro and in vivo.
CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC LTA subunits or (less prevalent) two LTA and one LTB subunits.
CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC associated (heterotrimers).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X01393; CAA25649.1; -
CC EMBL; X02911; CAA26670.1; -
CC EMBL; D00102; BAA00064.1; -
CC EMBL; M16441; BAA61199.1; -
CC EMBL; D12614; BAA02139.1; -
CC EMBL; M55913; AAB59455.1; -
CC EMBL; Z15026; CAA78746.1; -
CC EMBL; Y14768; CAA75071.1; -
CC EMBL; AF000505; BAB63397.1; -
CC EMBL; AF129756; AAD18092.1; -
CC EMBL; AY070490; AAL49956.1; -
CC EMBL; AY216498; AAO21135.1; -
CC EMBL; A06316; CAA00336.1; -
CC PIR; A92755; QMHUX.
CC PDB; 1TNR; 31-JUL-94.
CC GlycoSuiteDB; P01374; -
CC Genew; HGNC:6709; LTA.
CC MIM; 153440; -
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.


```

QY 72 ISPLVERGFORV-----AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 ISPLAQAGSSSRTPSKPVAHVVA-----NPQAEGL--QWLNERRANALLA 113
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 127 SNLHLRNGELVIEHKGFIYIYSOTYFRFQBEIKENTKNDKQMVQYIYKYT-----SYPD 180
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 NGVELRDNQLVWPSEGLYLIYSQVLFKQ-----GCPSTHVLTLTHTISRIAVSYQT 164
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 PILLMKSARNSCWSK-----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 165 KVNLLSAIKSPCORETPEGAEAPWIEPIYLGGVFQLEKGRDLSAEINRPDYLDFAESGQ 224
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 -PFG 238
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 225 VYFG 228
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: March 23, 2004, 09:14:18
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:11:14 ; Search time 45 Seconds
(without alignments)
1703.798 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYSKSGIACFL.....NEHLIDMDHEASFFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 520272

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvrius:*
- 16: sp_bacteriap:*
- 17: sp_archesp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	305.5	23.7	214	13	Q9DDZ5
2	175.5	13.6	169	11	Q9WV90
3	157	12.2	154	6	Q8MJ19
4	151.5	11.8	227	13	Q7T2Q3
5	144.5	11.2	216	11	Q70332
6	141	11.0	231	13	Q8AW02
7	137.5	10.7	232	11	Q80XA4
8	135	10.5	156	11	Q91ZL4
9	135	10.5	215	6	Q9BEE8
10	135	10.5	217	11	Q9PERG6
11	130.5	10.1	222	13	Q7T1U4
12	128	9.9	230	13	Q8JG37
13	126.5	9.8	225	13	Q91B42
14	125	9.7	215	11	Q9SND1
15	124	9.6	216	6	Q9BEC4
16	123.5	9.6	216	6	Q9BEC9

17	122	9.5	205	4	Q8N4C3
18	121.5	9.4	225	13	Q91B41
19	120	9.3	237	13	Q8AWC9
20	119	9.2	202	11	Q8OWE7
21	115.5	9.0	149	6	Q97543
22	110.5	8.6	217	6	Q9BEG0
23	110	8.5	93	6	Q9TTJ2
24	109.5	8.5	149	6	Q97538
25	109.5	8.5	149	6	Q9TTG8
26	108.5	8.4	214	6	Q9BEF3
27	108	8.4	103	6	Q864Y7
28	108	8.4	217	6	Q9BEG1
29	107	8.3	217	6	Q9BEF4
30	106.5	8.3	102	11	Q80Z06
31	105	8.2	138	6	Q9TTG7
32	103	8.0	216	6	Q9BEE0
33	99	7.7	217	6	Q9BEC5
34	98.5	7.7	102	11	Q80Z05
35	97.5	7.6	102	11	Q80Z04
36	97	7.5	174	4	Q81Z15
37	97	7.5	208	4	Q81Z16
38	93.5	7.3	102	11	Q80Z02
39	92.5	7.2	110	13	Q7ZZX5
40	92	7.1	103	6	Q864Z0
41	90.5	7.0	101	11	Q9R136
42	90.5	7.0	158	4	Q81Z14
43	88.5	6.9	102	11	Q80Z03
44	85.5	6.6	240	13	Q800J1
45	83	6.4	163	16	Q8XLG9

ALIGNMENTS

RESULT 1

Q9DDZ5 PRELIMINARY; PRT; 214 AA.

AC Q9DDZ5

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE TRAIL-like protein.

GN TNFSF10L.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Bobe J., Goetz F.W.;

RT "Molecular cloning and expression of a TNF receptor and two TNF

RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).

DR EMBL; AF250041; AAG47640.1; "

DR HSSP; P50591; 1D2Q.

DR ZFIN; ZDB-GENE-010801-1; tnfsf10l.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR006052; TNF family.

DR InterPro; IPR008983; TNF-like.

DR InterPro; IPR003636; TNF_subf.

DR Pfam; PF00229; TNF; 1.

DR ProDom; PD002012; TNF_subf; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS50049; TNF 2; 1.

SQ SEQUENCE 214 AA, 24033 MW; 98C00247AFF691AA CRC64;

Query Match: 23.7%; Score 305.5; DB 13; Length 214;
Best Local Similarity 37.6%; Pred. No. 1.1e-17;
Matches 62; Conservative 37; Mismatches 59; Indels 7; Gaps 3;


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OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Savan R., Sakai M.;
RT "Cloning of tumor necrosis factor 3 alpha in carp."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB112424; BAC7690.1;
SQ SEQUENCE 227 AA; 23226 MW; 010BC2B1E8D7265E CRC64;

Query Match
Best Local Similarity 11.0%; Score 151.5; DB 13; Length 227;
Matches 45; Conservative 34; Mismatches 68; Indels 31; Gaps 7;

QY 75 LVPRGQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWSSRSGHSFSLNHLRNG 134
Db 67 LSKENTSVKVAHLSGA-----YEPDVSKNIDWKONQDGAFFVSGGLKLVDR 113
QY 135 ELVIHKGFFYIYSQTYFRQBEIKENTKNDKQMVQVIYKTSYDP-----PILLMKSA 188
Db 114 EIIIPNDGIYFIYSQVSFHI--SKNDMTEDQEVHSHAVFYHSFFGIYKP--LIRAA 169
QY 189 RNSCW----SKDAEYGLSYIQGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
Db 170 RSACVHASNTEDVYD--TIYLGAFSLRAGDKLCTTTTELLPRVETDNAKTFEGVF 225

RESULT 5
O70332 PRELIMINARY; PRT; 216 AA.
ID AC O70332;
DT 01-AUG-1998 (T-EMBLrel. 07, Created)
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Tumor necrosis factor-alpha (fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis."
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL: AF046215; AAC40100.1;
DR HSSP: P06804; 2TNF.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR006053; TNF abc.
DR InterPro: IPR006052; TNF family.
DR InterPro: IPR008983; TNF-like.
DR InterPro: IPR003636; TNF_subf.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_subf; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
FT NON_TER 216
SQ SEQUENCE 216 AA; 23793 MW; BADA3F83F45B533 CRC64;

Query Match
Best Local Similarity 11.2%; Score 144.5; DB 11; Length 216;
Matches 45; Conservative 34; Mismatches 68; Indels 31; Gaps 7;

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Best Local Similarity 26.9%; Pred. No. 0.00032;
Matches 47; Conservative 28; Mismatches 63; Indels 37; Gaps 7;

QY 80 GPQVAAH---ITGTRGRSNTLSSPNSKNEKALGRKINS-----WSSRSGHSFSL 127
Db 49 GPQREKFPNPIIGMGQTLTLRSSQNSNDKPVGVVANHQVBOLEWLSHRALLAN 108
QY 128 NLHLRNGELVIHKGFFYIYSQTYFRQBEIKENTKNDKQMVQVIYK-----YTSYDP 180
Db 109 GMSLKDNLVIPADGLYLVYSQVLRGQ-----GCPSYVLLTHVTSRIASVYED 157
QY 181 PILLMKSAKNSCWSDAEYGV-----LYSIYOGGIFELKENDRIFVSVTNEHLID 229
Db 158 NYNLLSAIKSPC-PKETPEGEELKPWYEPYILGVGFQLEKGRLSAEVNLPKYLD 211

RESULT 6
O8AW02 PRELIMINARY; PRT; 231 AA.
ID AC O8AW02;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Putative tumour necrosis factor alpha two.
GN TNF-ALPHA2PRO.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Saeij J.P., Stet R.J., de Vries B., van Muiswinkel W.B.,
RA Wiegertjes G.F.;
RT "Molecular and functional characterization of carp TNF: Association of
RT TNF polymorphism with trypanotolerance."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ311801; CAC84642.2;
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR006053; TNF abc.
DR InterPro: IPR006052; TNF family.
DR InterPro: IPR008983; TNF like.
DR InterPro: IPR003636; TNF_subf.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_subf; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00049; TNF_2; 1.
SQ SEQUENCE 231 AA; 25927 MW; 2AD8871D0B1A82F1 CRC64;

Query Match
Best Local Similarity 11.0%; Score 141; DB 13; Length 231;
Matches 51; Conservative 38; Mismatches 90; Indels 40; Gaps 9;

QY 44 WLQRLVLRMILRTSEETISTVQEQQN-----ISPLVREGRGQVAAHITGR 92
Db 29 WRVCGVLLAVALCAAAAVCFGLTKNQNGGNALRLTLRDHLSKENVTSKVAIHLTGA- 87
QY 93 GRSNTLSSPNSKNEKALGRKINSWSSRSGHSFSLNHLRNGELVIHKGFFYIYSQTYF 152
Db 88 -----YDPDVCKDNL-----DMKQNDQAFVSGGLELVDRITIIIPNDGIYFVSQVF 135
QY 153 RFQBEIKENTKNDKQMV-----QYIKYTSYPPILLMKSAKNSC-WSKDAEYGLY-S 203
Db 136 HI--SKDHMTEDQVVMHSHAVLRYSESYGYPK---LFSAIRSACVHASSEDLWNT 190
QY 204 IYQGIGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
Db 191 IYLGAFNLRAEDRLRTETKELLPRVSENGKTFEGVF 229

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RESULT 7
Q80XA4 Q80XA4 PRELIMINARY; PRT; 232 AA.
AC Q80XA4;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Tumor necrosis factor precursor (Fragment).
GN TNF.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RN SEQUENCE FROM N.A.
RA Green R.M., Herbst M.M., Schountz T.;
RT "Cloning of the deer mouse tumor necrosis factor gene.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY249143; AAF03078.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR008983; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00449; TNF_2; 1.
DR NON_TER 1
FT SIGNAL
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 80 >232 tumor necrosis factor.
FT NON_TER 232 232
FT SEQUENCE 232 AA; 25704 MW; E48A9379DB4F216D CRC64;

Query Match 10.7%; Score 137.5; DB 11; Length 232;
Best Local Similarity 24.5%; Pred. No. 0.0013;
Matches 45; Conservative 36; Mismatches 78; Indels 25; Gaps 8;

Qy 72 ISPLVRRGQRVAHITGFRGRNTLSSPNSKNEKALGRKINS-----WESSRSG 122
Db 56 IGPOREKFPNNLP--IGSMAQTLLRSSQSSDKPVAHVAVHNVQVDSQLEWLSRRAN 113

Qy 123 HSFLSLNHLRNGELVIEHKGFIYYSQTYFRFQBEIKENTKNDKQWQYIYKY-TSYEDP 181
Db 114 ALLANGMDLKDNLQVLPADGLYLYVSQVLFKQ-----GCSNYVLLTHTVSRAVSVYEDK 168

Qy 182 ILLMKSARNCSWKDAEYG-----LYSIYGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
Db 169 VLLLSAITSKSPC-PKETPGSELKPWYEPYILGVGVQLEKGRLSAEVNHKPYLDFAESSGQ 227

Qy 236 -FFG 238
Db 228 VYFG 231

RESULT 8
Q91ZL4 Q91ZL4 PRELIMINARY; PRT; 156 AA.
AC Q91ZL4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.

Query Match 10.7%; Score 137.5; DB 11; Length 232;
Best Local Similarity 24.5%; Pred. No. 0.0013;
Matches 45; Conservative 36; Mismatches 78; Indels 25; Gaps 8;

Qy 72 ISPLVRRGQRVAHITGFRGRNTLSSPNSKNEKALGRKINS-----WESSRSG 122
Db 56 IGPOREKFPNNLP--IGSMAQTLLRSSQSSDKPVAHVAVHNVQVDSQLEWLSRRAN 113

Qy 123 HSFLSLNHLRNGELVIEHKGFIYYSQTYFRFQBEIKENTKNDKQWQYIYKY-TSYEDP 181
Db 114 ALLANGMDLKDNLQVLPADGLYLYVSQVLFKQ-----GCSNYVLLTHTVSRAVSVYEDK 168

Qy 182 ILLMKSARNCSWKDAEYG-----LYSIYGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
Db 169 VLLLSAITSKSPC-PKETPGSELKPWYEPYILGVGVQLEKGRLSAEVNHKPYLDFAESSGQ 227

Qy 236 -FFG 238
Db 228 VYFG 231

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OX NCBI_TaxID=42415;
RN [1]
RN SEQUENCE FROM N.A.
RA Blanco J.C., Pletneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF421388; AAL18818.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00449; TNF_2; 1.
DR NON_TER 1
FT SIGNAL
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 80 >232 tumor necrosis factor.
FT NON_TER 232 232
FT SEQUENCE 156 AA; 17303 MW; DC565F3BC3C826E4 CRC64;

Query Match 10.5%; Score 135; DB 11; Length 156;
Best Local Similarity 23.5%; Pred. No. 0.0013;
Matches 43; Conservative 33; Mismatches 67; Indels 40; Gaps 8;

Qy 65 VQEKQONISPLVRRGQRVAHITGFRGRNTLSSPNSKNEKALGRKINSWESSRSGHS 124
Db 1 LRSSSQNLSS-----DKPVAHVVA-----NQABEQL-----EWLSQRANAL 36

Qy 125 FLSNHLRNGELVIEHKGFIYYSQTYFRFQBEIKENTKNDKQWQYIYK--YTSYDPDI 182
Db 37 LANGMDLRNQLVLPADGLYLYVSQVLF-----KGLGRNCELLTHTVSRIAVSVYEDKV 90

Qy 183 ILLMKSARNCSWKDAEYG-----LYSIYGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235
Db 91 VLLLSAITSKSPC-PKETPGSELKPWYEPYILGVGVQLEKGRLSAEVNHKPYLDFAESSGQV 149

Qy 236 FFG 238
Db 150 YFG 152

RESULT 9
Q9BE8 Q9BE8 PRELIMINARY; PRT; 215 AA.
AC Q9BE8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Erinaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RN SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are their sister group.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286830; CAC28522.1; -.
DR HSSP; P01375; 4TSV.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.

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DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 230 AA; 25598 MW; 3A40D391F75DB019 CRC64;

Query Match
Best Local Similarity 9.8%; Score 128; DB 13; Length 230;
Matches 37; Conservative 25; Mismatches 53; Indels 12; Gaps 5;

QY 124 SFLSNHLRNGELVIEHKGFIYISQYFRFQEEIKENTKNDKQMVQYIYKTSYDPPIL 183
D 104 SFSGLKLENEIKILRDGLYFVYSQASYRLCK-AGDETEGEVHMVKVRSWSDSYS 162
QY 184 -----LMKSARNCSWDAEYGLY----SIYGGIFELKENDRIFVSVTNEHLIDMDEHA-- 234
D 163 SWKPLLSATRSACKTTEYQKYWGAVILGAAFLNKAGDRL-RTVMDEXLKPVESAGG 221
QY 235 -SPFGAF 240
D 222 KTFPGTF 228

RESULT 13
Q9IB42
ID Q9IB42 PRELIMINARY; PRT; 225 AA.
AC Q9IB42;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20491932; PubMed=11035080;
RA Harono I., Nam B., Kurobe T., Aoki T.;
RT "Molecular Cloning, Characterization, and Expression of TNF cDNA and
RL Gene from Japanese Flounder Paralicthys olivaceus.";
RL J. Immunol. 165:4423-4427(2000).
DR EMBL; AB040448; BAA94969.1; -.
DR HSSP; P01375; 4TSV.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 225 AA; 24965 MW; 8F947B25FC82658 CRC64;

Query Match
Best Local Similarity 9.8%; Score 126.5; DB 13; Length 225;
Matches 42; Conservative 40; Mismatches 78; Indels 31; Gaps 8;

QY 67 EKQNISPLVRGPQVAAHITGRGRSNTLSPNS---KNEKALGRKINSWESSRSGH 123

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Db 47 EXTEPHNTLRQISSRAAAIHLEG-RDEDETSNKLYWKNDGLA-----FTQGGF 98
QY 124 SFLSNHLRNGELVIEHKGFIYISQYFRFQ-----EEIKENTKNDKQMVQY-IYKYT 176
D 99 ELVDN-----HIIIPRGLYFVYSQASFRVSCSSDDADDGKAAEKHLTSSHRVWLET 152
QY 177 -SYDDPILLMKSGARNCSW-----KDAEYGLYISYGGIFELKENDRIFVSVTNEHLID 229
D 153 ESLGTQVSLMSAVRSACQSQEDAYRDGGQWYNAILGAVFQNLNMGDKLWTETNMLSELE 212
QY 230 MDHEASEFFCAF 240
D 213 TSGKTFFGVF 223

RESULT 14
Q99ND1
ID Q99ND1 PRELIMINARY; PRT; 215 AA.
AC Q99ND1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Tamiasciurus hudsonicus (American red squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scurinae;
OC Tamiasciurus.
OX NCBI_TaxID=10009;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286824; CAC28540.1; -.
DR HSSP; P06804; 2TNF.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23739 MW; 36441309CA5E9898 CRC64;

Query Match
Best Local Similarity 9.7%; Score 125; DB 11; Length 215;
Matches 35; Conservative 29; Mismatches 62; Indels 18; Gaps 4;

QY 99 SSPNSKNEKALGRKINS-----WESSRSGHSFTLNHLRNGELVIEHKGFIYISQY 151
D 71 SSSQNMNDKFAHVAVANQTEQLQWLSRRANALLANGMELIDNLVVPADGLYISQVL 130
QY 152 FRFQEEIKENTKNDKQMVQYIYKY-TSYDDPILLMKSGARNCSWDAEYGLYS-----IY 205
D 131 FKQG-----GCSSYVLLTHTVSRFAVSQDKVKNLLSATKSPCKSLGAEKPKWYEPIY 185
QY 206 QGGIFELKENDRIFVSVTNEHLID 229
D 186 LGGVFELOKGDRLSAEVLNLPVILD 209

RESULT 15

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Search completed: March 23, 2004, 09:15:15
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:04:03 ; Search time 23 Seconds
(without alignments)
630.735 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMEVQGSLSGTCVLIV.....NEHLMDHREASFFGAPLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A COMB.pap.*

2: /cgn2_6/ptodata/2/iaa/5B COMB.pap.*

3: /cgn2_6/ptodata/2/iaa/6A COMB.pap.*

4: /cgn2_6/ptodata/2/iaa/6B COMB.pap.*

5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pap.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	1	US-08-670-354-2
2	1478	100.0	281	3	US-08-584-031-1
3	1478	100.0	281	3	US-08-780-496-1
4	1478	100.0	281	3	US-08-893-086-10
5	1478	100.0	281	3	US-08-320-424-2
6	1478	100.0	281	4	US-09-333-593A-6
7	1478	100.0	281	4	US-09-157-864-11
8	1478	100.0	281	4	US-09-825-563-2
9	1478	100.0	281	4	US-10-039-785-66
10	1478	100.0	281	5	PCT-US96-10895-2
11	1469	99.4	279	4	US-09-072-993C-3
12	988	66.8	253	3	US-09-320-424-11
13	988	66.8	253	4	US-09-825-563-11
14	988	66.8	256	3	US-09-320-424-13
15	988	66.8	256	4	US-09-825-563-13
16	930	62.9	177	3	US-09-105-343A-7
17	930	62.9	291	1	US-08-670-354-6
18	930	62.9	291	3	US-08-320-424-6
19	930	62.9	291	4	US-09-825-563-6
20	930	62.9	291	5	PCT-US96-10895-6
21	850	57.5	161	4	US-09-565-423-7
22	654	44.2	183	3	US-09-105-343A-8
23	482	32.6	101	1	US-08-670-354-4
24	482	32.6	101	3	US-09-320-424-4
25	482	32.6	101	4	US-09-825-563-4
26	482	32.6	101	5	PCT-US96-10895-4
27	446	30.2	85	4	US-09-632-287A-12

28	258.5	17.5	294	3	US-08-996-139-11	Sequence 11, Appl
29	258.5	17.5	294	3	US-08-995-659-11	Sequence 11, Appl
30	258.5	17.5	294	3	US-09-215-649A-11	Sequence 11, Appl
31	258.5	17.5	294	4	US-09-577-780-11	Sequence 11, Appl
32	258.5	17.5	294	4	US-09-577-800-11	Sequence 11, Appl
33	258.5	17.5	294	4	US-09-466-496-11	Sequence 11, Appl
34	258.5	17.5	294	4	US-09-871-856-11	Sequence 11, Appl
35	258.5	17.5	294	4	US-09-871-291-11	Sequence 11, Appl
36	258.5	17.5	294	4	US-09-877-650-11	Sequence 11, Appl
37	258.5	17.5	316	2	US-08-842-842-7	Sequence 7, Appl
38	258.5	17.5	316	3	US-08-989-362-2	Sequence 2, Appl
39	258.5	17.5	316	4	US-09-052-521C-2	Sequence 2, Appl
40	258.5	17.5	316	4	US-09-671-658A-2	Sequence 2, Appl
41	258.5	17.5	316	4	US-09-396-937-4	Sequence 4, Appl
42	258.5	17.5	316	4	US-09-396-937-6	Sequence 6, Appl
43	251.5	17.0	317	3	US-08-996-139-13	Sequence 13, Appl
44	251.5	17.0	317	3	US-08-995-659-13	Sequence 13, Appl
45	251.5	17.0	317	3	US-09-215-649A-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

Query Match 100.0%; Score 1478; DB 1; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120
Db 61 DDSYDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 2
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669-220S03
; CURRENT APPLICATION NUMBER: US/08/584.031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60

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QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 3
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim

Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120
Db 61 DDSYDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 4
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA

Best Local Similarity 100.0%; Score 1478; DB 3; Length 281;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120
Db 61 DDSYDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

TITLE OF INVENTION: APO-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-3881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-780-496-1

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; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembecki, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
; US-08-883-086-10

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSNRSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSNRSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFVLG 281

RESULT 5
US-09-320-424-2
; Sequence 2, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-09-320-424-2

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSNRSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSNRSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFVLG 281

RESULT 6
US-09-333-593A-6
; Sequence 6, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 281
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-333-593A-6

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
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; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembecki, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
; US-08-883-086-10

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSNRSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSNRSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFVLG 281

RESULT 6
US-09-333-593A-6
; Sequence 6, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 281
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-333-593A-6

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
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QY 61 DDSYDNDPDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVRERGQ 120
DB 61 DDSYDNDPDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7

US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-157-864-11

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGSIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGSIACFLKE 60
QY 61 DDSYDNDPDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVRERGQ 120
DB 61 DDSYDNDPDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8

US-09-825-563-2
; Sequence 2, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-B
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-09-825-563-2

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGSIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGSIACFLKE 60
QY 61 DDSYDNDPDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVRERGQ 120
DB 61 DDSYDNDPDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 9

US-10-039-785-66
; Sequence 66, Application US/10039785

Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PE550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 66
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-10-039-785-66

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMVEVGGPSLGQTCLVIFVTLQSLCAVAVYVYFNLKQMDKYSGKIACFLKE 60
DB 1 MAMVEVGGPSLGQTCLVIFVTLQSLCAVAVYVYFNLKQMDKYSGKIACFLKE 60
QY 61 DSYWDPNDEESNPSQWQVQKQLRQLVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120
DB 61 DSYWDPNDEESNPSQWQVQKQLRQLVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 10
PCT-US96-10895-2
Sequence 2, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match 100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMVEVGGPSLGQTCLVIFVTLQSLCAVAVYVYFNLKQMDKYSGKIACFLKE 60
DB 1 MAMVEVGGPSLGQTCLVIFVTLQSLCAVAVYVYFNLKQMDKYSGKIACFLKE 60
QY 61 DSYWDPNDEESNPSQWQVQKQLRQLVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120
DB 61 DSYWDPNDEESNPSQWQVQKQLRQLVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 11
US-09-072-993C-3
Sequence 3, Application US/09072993C
Patent No. 6346388
GENERAL INFORMATION:
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
FILE REFERENCE: GH-50030
CURRENT APPLICATION NUMBER: US/09/072,993C
CURRENT FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/056,980

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; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-3

Query Match
  99.4%; Score 1469; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.5e-148;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVQGGPSLQTCVLIVIFVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKEDD 62
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QY 63 SYWDPNDESMNCPQWQVQWQLQVVKMLRTSEETISTVQEKQONISPLVRGPQV 122
Db 61 SYWDPNDESMNCPQWQVQWQLQVVKMLRTSEETISTVQEKQONISPLVRGPQV 120

QY 123 AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKGFY 182
Db 121 AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKGFY 180

QY 183 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYDPDPILLMKSARNSCWSKDAEYGLYSI 242
Db 181 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYDPDPILLMKSARNSCWSKDAEYGLYSI 240

QY 243 YQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 YQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 279

RESULT 12
US-09-320-424-11
; Sequence 11, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; PRIOR FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-11

Query Match
  66.8%; Score 988; DB 3; Length 253;
Best Local Similarity 78.9%; Pred. No. 4.3e-97;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

QY 39 TNELKQMDKYSGIACFLKEDDSYWDPNDESMNCPQWVK---WQLRQLVRKMLRT 95
Db 29 SDRMKQIEDKI-----EILSKIYHIENETARIKKLIGERTST 67

QY 96 SEETISTVQEKQONISPLVRGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSWE 155
Db 68 SEETISTVQEKQONISPLVRGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSWE 127

QY 156 SRSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVYIYKTS 215
Db 128 SRSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVYIYKTS 187

QY 216 YPDPIILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFSVTNEHLIDMDHEASFF 275
Db 188 YPDPIILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFSVTNEHLIDMDHEASFF 247

QY 276 GAFLVG 281
Db 248 GAFLVG 253

Query Match
  66.8%; Score 988; DB 4; Length 253;
Best Local Similarity 78.9%; Pred. No. 4.3e-97;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

QY 39 TNELKQMDKYSGIACFLKEDDSYWDPNDESMNCPQWVK---WQLRQLVRKMLRT 95
Db 29 SDRMKQIEDKI-----EILSKIYHIENETARIKKLIGERTST 67

QY 96 SEETISTVQEKQONISPLVRGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSWE 155
Db 68 SEETISTVQEKQONISPLVRGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSWE 127

QY 156 SRSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVYIYKTS 215
Db 128 SRSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVYIYKTS 187

QY 216 YPDPIILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFSVTNEHLIDMDHEASFF 275
Db 188 YPDPIILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFSVTNEHLIDMDHEASFF 247

QY 276 GAFLVG 281
Db 248 GAFLVG 253
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RESULT 14

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US-09-320-424-13
; Sequence 13, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,045
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-13

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RESULT 15

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RES001 15
US-09-825-563-13
; Sequence 13, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 05/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25

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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:06:53 ; Search time 46 Seconds
(without alignments)

1581.879 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

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Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1478	100.0	281	8	US-08-916-625B-6
2	1478	100.0	281	8	US-08-971-317A-8
3	1478	100.0	281	9	US-09-813-329-17
4	1478	100.0	281	9	US-09-193-663-8
5	1478	100.0	281	9	US-09-334-465-1
6	1478	100.0	281	10	US-09-919-039-118
7	1478	100.0	281	12	US-10-202-062-20
8	1478	100.0	281	12	US-10-662-429-2
9	1478	100.0	281	12	US-10-662-430-2
10	1478	100.0	281	12	US-10-662-431-2
11	1478	100.0	281	13	US-10-039-785-66
12	1478	100.0	281	13	US-10-011-125-4
13	1478	100.0	281	13	US-10-001-054-54
14	1478	100.0	281	14	US-10-093-766-54
15	1478	100.0	281	14	US-10-174-654-11

16	1478	100.0	281	14	US-10-151-882-41
17	1478	100.0	281	14	US-10-218-547-20
18	1478	100.0	281	14	US-10-322-673-72
19	1478	100.0	281	14	US-10-139-785-66
20	1478	100.0	281	14	US-10-310-793-26
21	1478	100.0	281	15	US-10-292-486-5
22	1478	100.0	281	15	US-10-333-712-1
23	1469	99.4	279	13	US-10-066-209-3
24	1269.5	85.9	246	9	US-09-855-544A-13
25	1017	68.8	208	9	US-09-855-544A-16
26	985.5	66.7	461	12	US-10-389-223A-6
27	982	66.4	480	12	US-10-389-223A-4
28	978	66.2	614	12	US-10-389-223A-2
29	964.5	65.3	296	14	US-10-185-425-5
30	937.5	63.4	188	9	US-09-855-544A-14
31	930	62.9	291	10	US-09-873-829-6
32	930	62.9	291	13	US-10-017-910-6
33	887	60.0	168	9	US-09-900-530A-10
34	878	59.4	166	9	US-09-779-050A-16
35	859	58.1	164	13	US-10-116-378-29
36	850	57.5	161	14	US-10-216-074-7
37	849	57.4	161	14	US-10-338-083-11
38	836	43.0	172	9	US-09-779-050A-17
39	561	38.0	113	9	US-09-855-544A-15
40	482	32.6	98	9	US-09-855-544A-9
41	468	31.7	88	9	US-09-855-544A-10
42	446	30.2	85	14	US-10-286-696-12
43	278	18.8	56	15	US-10-399-018-20
44	258.5	17.5	294	9	US-09-871-856-11
45	258.5	17.5	294	9	US-09-877-650-11

ALIGNMENTS

RESULT 1

US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Publication NO. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; TITLE OF INVENTION: RECEPTOR, TR6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50008-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701

TELEX: 846169
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-916-6259-6

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNKLKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNKLKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
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QY 181 FYIYSQTYFRFOEBIKENTKNDKQVQYIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
DB 181 FYIYSQTYFRFOEBIKENTKNDKQVQYIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
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DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 2
US-08-971-317A-8
; Sequence 8, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,317A
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mimi C
; REGISTRATION NUMBER: 39,046
; REFERENCE/DOCKET NUMBER: 6255.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-8

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNKLKQMDKYKSGIACFLKE 60
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QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
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DB 181 FYIYSQTYFRFOEBIKENTKNDKQVQYIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
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DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 3
US-09-813-329-17
; Sequence 17, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mol
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-17

Query Match 100.0%; Score 1478; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNKLKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
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DB 181 FYIYSQTYFRFOEBIKENTKNDKQVQYIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 4

US-09-193-663-8
 ; Sequence 8, Application US/09193663
 ; Patent No. US20020055624A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wiley, Steven R.
 ; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
 ; FILE REFERENCE: 6255-US-02
 ; CURRENT APPLICATION NUMBER: US/09/193,663
 ; CURRENT FILING DATE: 1998-11-17
 ; EARLIER APPLICATION NUMBER: 60/065,916
 ; EARLIER FILING DATE: 1997-11-17
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-193-663-8

Query Match 100.0%; Score 1478; DB 9; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYVYFTNELKOMQDKYSKSGIACFLKE 60
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 Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
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 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
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 Db 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSNCSWCKDAEYGLY 240
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RESULT 5

US-09-934-465-1
 ; Sequence 1, Application US/09934465
 ; Patent No. US20020102233A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: APO-2 LIGAND
 ; FILE REFERENCE: 11669.22US03
 ; CURRENT APPLICATION NUMBER: US/09/934,465
 ; CURRENT FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: 08/584,031
 ; PRIOR FILING DATE: 1996-01-09
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-934-465-1

Query Match 100.0%; Score 1478; DB 9; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYVYFTNELKOMQDKYSKSGIACFLKE 60
 |||||
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYVYFTNELKOMQDKYSKSGIACFLKE 60
 |||||
 QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 |||||
 Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 |||||
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 |||||
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 |||||
 QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSNCSWCKDAEYGLY 240
 |||||
 Db 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSNCSWCKDAEYGLY 240
 |||||
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 |||||
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 |||||

RESULT 6

US-09-919-039-118
 ; Sequence 118, Application US/09919039
 ; Publication No. US20030108871A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 ; FILE REFERENCE: PA-0035 US
 ; CURRENT APPLICATION NUMBER: US/09/919,039
 ; CURRENT FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: 60/222,113
 ; PRIOR FILING DATE: 2000-07-28
 ; NUMBER OF SEQ ID NOS: 401
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 118
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030108871A1 0595090CD1
 US-09-919-039-118

Query Match 100.0%; Score 1478; DB 10; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYVYFTNELKOMQDKYSKSGIACFLKE 60
 |||||
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYVYFTNELKOMQDKYSKSGIACFLKE 60
 |||||
 QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 |||||
 Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 |||||
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 |||||
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 |||||
 QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSNCSWCKDAEYGLY 240
 |||||
 Db 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSNCSWCKDAEYGLY 240
 |||||
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 |||||
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 |||||

RESULT 7

US-10-202-062-20
 ; Sequence 20, Application US/10202062

```
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-10-202-062-20

Query Match      100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60
DB      1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60

QY      61 DDSYWDNDDEESMNSPCQVQKQRLQVVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB      61 DDSYWDNDDEESMNSPCQVQKQRLQVVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

QY      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY      181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB      181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 8
US-10-662-429-2
; Sequence 2, Application US/10662429
; Publication No. US20040038347A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,429
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8512
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-10-202-062-20

Query Match      100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60
DB      1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60

QY      61 DDSYWDNDDEESMNSPCQVQKQRLQVVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB      61 DDSYWDNDDEESMNSPCQVQKQRLQVVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

QY      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY      181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB      181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 9
US-10-662-430-2
; Sequence 2, Application US/10662430
; Publication No. US20040048340A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,430
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 281 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-662-430-2

Query Match 100.0%; Score 1478; DB 12; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-10-662-431-2

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNIPLVRERGQ 120
 DB 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNIPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281

RESULT 10

US-10-662-431-2
 ; Sequence 2, Application US/10662431
 ; Publication No. US20040047864A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben, Steven M
 ; TITLE OF INVENTION: Apoptosis Inducing Molecule I
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/662,431
 ; FILING DATE: 16-Sep-2003
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/816,981
 ; FILING DATE: 13-MAR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kimball, Paul, C.
 ; REGISTRATION NUMBER: 34,610
 ; REFERENCE/DOCKET NUMBER: PF261
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-662-431-2

Query Match 100.0%; Score 1478; DB 12; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-10-662-431-2

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNIPLVRERGQ 120
 DB 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNIPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281

RESULT 11

US-10-039-785-66
 ; Sequence 66, Application US/10039785
 ; Publication No. US20020067846A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Salcedo et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
 ; FILE REFERENCE: PF550
 ; CURRENT APPLICATION NUMBER: US/10/039,785
 ; CURRENT FILING DATE: 2002-05-07
 ; PRIOR APPLICATION NUMBER: 60/369,860
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: 60/341,237
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: 60/331,310
 ; PRIOR FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,044
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: 60/327,364
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/323,807
 ; PRIOR FILING DATE: 2001-09-21
 ; PRIOR APPLICATION NUMBER: 60/309,176
 ; PRIOR FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/294,981
 ; PRIOR FILING DATE: 2001-06-04
 ; PRIOR APPLICATION NUMBER: 60/293,473
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 66
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-039-785-66

Query Match 100.0%; Score 1478; DB 13; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-10-039-785-66

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNIPLVRERGQ 120

```
Db 61 DSDYDPNDESNMPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
QY 181 FYIYSOTYFRFOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYSOTYFRFOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 12
US-10-011-125-4
; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: F1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4

Query Match 100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANVEQGGSLGTCVLIVFTVLQSLCAVAVYVFTNELKQMDQKYSKGIACFLKE 60
Db 1 MANVEQGGSLGTCVLIVFTVLQSLCAVAVYVFTNELKQMDQKYSKGIACFLKE 60
QY 61 DSDYDPNDESNMPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSDYDPNDESNMPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
QY 181 FYIYSOTYFRFOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYSOTYFRFOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 13
US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Shelton, David
```

```
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/096891
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/096894
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100263
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/107783
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112420
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/115554
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116533
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/131294
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/180997
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; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/218517
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/284291
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380913
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 09/403297
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/423741
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/802706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/866034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/882636
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/928404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US99/00106
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/08615
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28634
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00376
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/06884
; PRIOR FILING DATE: 2000-03-15

; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/13705
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/14941
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/22031
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US01/27099
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-54

Query Match 100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAMMEVGGPSLGTQCVLIIVFTVLLQSLCAVATYVYFTNELKQMDKYSKSGIACFLKE	60
Db	1	MAMMEVGGPSLGTQCVLIIVFTVLLQSLCAVATYVYFTNELKQMDKYSKSGIACFLKE	60
Qy	61	DDSYWDPNDEESMNSPCWQVKWLRLQVRKMLRTSEETISTYVQEKQNISPLVRERGPO	120
Db	61	DDSYWDPNDEESMNSPCWQVKWLRLQVRKMLRTSEETISTYVQEKQNISPLVRERGPO	120
Qy	121	RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSLNHLNGLVTHEKG	180
Db	121	RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSLNHLNGLVTHEKG	180
Qy	181	FYIYSQTYPRFQEEIKENTKNDKQWQYIYKYVTSYDPDILLMKSNRSCWSDAEVGLY	240
Db	181	FYIYSQTYPRFQEEIKENTKNDKQWQYIYKYVTSYDPDILLMKSNRSCWSDAEVGLY	240
Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG	281
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG	281

RESULT 14

US-10-093-766-54
; Sequence 54, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.

APPLICANT: Karpf, Adam R.
TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
FILE REFERENCE: PA-0047 US
CURRENT APPLICATION NUMBER: US/10/093,766
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program
SEQ ID NO 54
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDNDDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 15
US-10-174-654-11
Sequence 11, Application US/10174654
Publication No. US20030044937A1
GENERAL INFORMATION:
APPLICANT: Bienkowski, Michael J
Mills, Cynthia J
Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
Legal Services
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,654
FILING DATE: 19-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-174-654-11

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDNDDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Search completed: March 23, 2004, 09:12:35
Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:04:03 ; Search time 21 Seconds

(without alignments)
1287.134 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMEVQGGPSLQTCVLIV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189.5	12.8	279	2 A53062	Fas ligand - mouse
2	186	12.6	281	2 I38707	Fas ligand - human
3	177.5	12.0	278	2 A49266	Fas ligand - rat
4	164	11.1	261	2 S53090	CD40 ligand - bovi
5	147.5	10.0	261	2 I53476	CD40 ligand - huma
6	141	9.5	234	1 A25451	tumor necrosis fac
7	141	9.5	260	2 S21738	CD40 ligand - mous
8	134.5	9.1	204	1 S17289	tumor necrosis fac
9	133	9.0	232	1 S12606	tumor necrosis fac
10	131.5	8.9	233	1 S22052	tumor necrosis fac
11	131	8.9	234	1 JQ1344	tumor necrosis fac
12	130.5	8.8	233	1 S24642	tumor necrosis fac
13	129.5	8.8	235	2 I54490	tumor necrosis fac
14	127.5	8.6	204	1 S24641	lymphotoxin - bovi
15	125.5	8.5	233	1 QWHUN	tumor necrosis fac
16	123.5	8.4	235	1 QWMSN	tumor necrosis fac
17	123.5	8.4	235	2 JU0029	tumor necrosis fac
18	122	8.3	205	1 QWHUX	lymphotoxin alpha
19	121	8.2	234	1 JH0529	tumor necrosis fac
20	115.5	7.8	193	2 S06192	tumor necrosis fac
21	114	7.7	202	1 B27303	tumor necrosis fac
22	113.5	7.7	195	2 S52715	tumor necrosis fac
23	113.5	7.7	306	2 I49139	lymphotoxin-beta -
24	112.5	7.6	638	1 QQB2M	mRNA maturase b14
25	111.5	7.5	202	1 JN0869	tumor necrosis fac
26	109	7.4	652	2 I48083	amphotropic murine
27	107	7.2	197	1 JH0309	tumor necrosis fac
28	102	6.9	244	2 A46066	lymphotoxin beta -
29	100	6.8	865	2 AB1658	probable membrane

30	99.5	6.7	233	2 S11688	tumor necrosis fac
31	97.5	6.6	448	2 F95122	protein kinase, pr
32	95	6.4	345	2 T14707	DNA ligase homolog
33	95	6.4	365	2 T15010	hypothetical prote
34	95	6.4	455	2 G95104	hypothetical prote
35	94.5	6.4	4981	2 T18489	hypothetical prote
36	94	6.4	1465	2 T23056	chromodomain helic
37	92.5	6.3	833	1 A31593	heat shock transcr
38	92.5	6.3	1538	2 T29095	cardiac muscle fac
39	91	6.2	1176	2 JN0583	myosin-light-chain
40	90.5	6.1	502	2 A53444	actinin receptor-1
41	90.5	6.1	502	2 JC2491	serine/threonine k
42	90.5	6.1	1284	2 T40578	hypothetical prote
43	90	6.1	907	2 E96636	hypothetical prote
44	89.5	6.1	313	2 T03031	NBS-LRR type resis
45	89	6.0	328	2 B59296	alpha-N-arabinofur

ALIGNMENTS

RESULT 1

A53062

Fas ligand - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C/Accession: A53062

R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Na Cell 76, 969-976, 1994

A>Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in A:Reference number: A53062; MUID:94185175; PMID:7511063

A:Accession: A53062

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-279 <TAK>

A:Cross-references: GB:U06948; NID:g473564; PTDN:AAAL7800.1; PID:g473565

Query Match 12.8%; Score 189.5; DB 2; Length 279;

Best Local Similarity 25.8%; Pred. No. 1.5e-08;

Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

QY 83 QIRQLVRKMLRTSETISTVQEKQONISPLVRERGPQVAAHITGTGRSNTLSPNSK 142

Db 111 ELREFTNQSL-----KVSSPEKQIANPSTPEKKEPRSV-AHLTG-----NPHSR 154

QY 143 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEKGFYIYSQTYRFRQBEIKENTKN 202

Db 155 SIPL-----EWEDT-YGTALISGVKYGKGLVINETGLYFYVKYVFRGQ-----SCN 201

QY 203 DKQMVQYIY-KYTSYPPDPILLMKSR--NSCWSKDAEYGLYSIQGIFELKENDRIFVSV 260

Db 202 NQPLNHKVYMRNSKYPEDLVLMEEKELNYCTI--QGIWAHSSYLGAVFNLTSADHLYVNI 259

QY 261 TNEHLIDMDHEASFGAFLVG 278

Db 260 SOLSLINFEESKTFRGLY 277

RESULT 2

I38707

Fas ligand - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C/Accession: I38707; S57565; I38554

R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

Int. Immunol. 6, 1567-1574, 1994

A>Title: Human Fas ligand: gene structure, chromosomal location and species specificity

A:Reference number: I38707; MUID:95127560; PMID:7826947

A:Accession: I38707

A>Status: preliminary; translated from GB/EMBL/DBDJB

A:Molecule type: mRNA

A:Residues: 1-281 <RES>

A:Cross-references: EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431

R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994
 A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
 A;Reference number: JC2340; MUID:95071350; PMID:7980502
 A;Accession: JC2340
 A;Molecule type: DNA
 A;Residues: 1-281 <MUT>
 A;Cross-references: GB:D38122; DDBJ:D29820; NID:G601892; PIDN:BAA07320.1; PID:gl369902
 R;Schatzlein, C.E.
 A;Reference number: S57565
 A;Accession: S57565
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-281 <SCH>
 A;Cross-references: EMBL:X89102; NID:G887455; PID:G887456
 R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G.J. Exp. Med. 181, 71-77, 1995
 A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
 A;Reference number: I38554; MUID:95105731; PMID:7528780
 A;Accession: I38554
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-281 <RE2>
 A;Cross-references: EMBL:U08137; NID:G624627; PIDN:AAC50071.1; PID:G624628
 C;Genetics:
 A;Gene: FasL
 A;Introns: 151/1; 116/3
 C;Keywords: glycoprotein; transmembrane protein
 F;80-102/Domain: transmembrane #status predicted <TM>
 F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 186; DB 2; Length 281;
 Best Local Similarity 22.4%; Pred. No. 3.1e-08;
 Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;
 QY 4 MEYGGPSLQGTCLVIFVLLQSLCAV--TYVFTNELKQMDKYKSGIACFLKE 60
 Db 71 LKXGNHSTG-LCLLVNFFVVALVGLGCMQLFHLQKELAELESTQMTASLEK 129
 QY 61 DSYWPNDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQNTISPLVRBGPQ 120
 Db 130 QIGHPSPPPE-----KXELRV----- 146
 QY 121 RVAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSHSFLSNLHLRNGELVTHEKG 180
 Db 147 ---AHLT---GKNSRSM-----LEWET-YGIVLLSGVKYKGLGVINETG 187
 QY 181 FYIYSQTYPRFOEIKENTKNDKQVQIY-KYTSYPPDPILLMKGARN-----CWSK 233
 Db 188 LYFVSKYVFRGQ-----SCNNLPLSHKVMNSKYPQDLVMEGKWMKSYCTTGQWVAR 241
 QY 234 DAEGYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 Db 242 -----SSYLGAFAVNLTSADHLVYVNSLSLVNFEESQTFFGLY 279

RESULT 3
 A49266
 fas ligand - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: A49266
 R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
 Cell 75, 1169-1178, 1993
 A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
 A;Reference number: A49266; MUID:94084792; PMID:7505205
 A;Accession: A49266
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-278 <SD>
 A;Cross-references: GB:U003470; NID:G440178; PIDN:AAC52129.1; PID:G440179
 C;Keywords: glycoprotein; transmembrane protein

Query Match 12.0%; Score 177.5; DB 2; Length 278;
 Best Local Similarity 27.5%; Pred. No. 1.6e-07;
 Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;
 QY 100 ISTVQEKQONISPLVRBGPQVAAHITCT-RGRSNTLSSPNKNEKALGRKINSWESSR 158
 Db 121 VSSFEKQIANPSTPSTKPRSV-AHLTGNPRSRISPL-----EWEDT- 162
 QY 159 SGHSFLSNLHLRNGELVTHEKGFYIYSQTYPRFOEIKENTKNDKQVQIY-KYTSY 217
 Db 163 YGTALISGVKYYKGLVINEAGLYFYVSKYVFRGQ-----SCNSQPLSHKVMNRKPY 216
 QY 218 DPILLMKSR-NSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
 Db 217 GDVLVMEKKLVCTI--CQIWAHSSYLGAVENLTVADHLVYNISQSLINFEESKTFFG 274
 QY 277 AF 278
 Db 275 LY 276

RESULT 4
 S53090
 CD40 ligand - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
 C;Accession: S53090
 R;Mertens, B.E.L.C.; Muriuki, M.
 submitted to the EMBL Data Library, February 1995
 A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
 A;Reference number: S53090
 A;Accession: S53090
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-261 <NER>
 A;Cross-references: EMBL:Z48469; NID:G732569; PIDN:CAA89363.1; PID:G732570

Query Match 11.1%; Score 164; DB 2; Length 261;
 Best Local Similarity 25.9%; Pred. No. 2.1e-06;
 Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;
 QY 6 VGGPSLQGTCLVIFVTL--QSLCAVAVTVYFTNELKQMDKYKSGIACFLKEDDS 63
 Db 13 VATGPVSMK-IFMYLLTVFLITQMGSAFVALHRLDKIEDERNLHEDFVFMK--T 68
 QY 64 YWDPNDEESMNS--PCQVKQLRQLVRKMLRTSEETISTVQEKQNTISPLVRBGPOR 121
 Db 69 IQRCNKGEGLSLLNCEIRSFEDLV-KDINQKE-----VKKKEKFMHKGQDEPO- 121
 QY 122 VAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSHSFLSN--LHLRNG-ELVTHE 178
 Db 122 IAAHV-----ISEASSKTTSVL-----QW--APKGYVTLNNLVTLENGKQLAVKR 165
 QY 179 KGFYIYSQTYPRFOEIKENTKNDKQVQIYKYTSYPPDPILLMKSRNSCWSKDAEYG 238
 Db 166 QGYFYIYQVTFCSNRE-----TLQAPFIASLCLKSPSGSERILLRAANTHSSSKPC--G 219
 QY 239 LYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
 Db 220 QQSILHGGVFELOSGASVFNVTDPSSQVSHGTGFTSFG 257

RESULT 5
 I53476
 CD40 ligand - human
 N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
 C;Species: Homo sapiens (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
 C;Accession: S28017; JH0793; S26852; S2852; I53476; S25684; S30593
 R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;
 EMBO J. 11, 4313-4321, 1992
 A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand fo

R:Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi,
DNA 5, 149-156, 1986
A>Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for xae
A:Reference number: A25454; MUID:86219711; PMID:3519137
A:Accession: A25454
A:Molecule type: mRNA
A:Residues: 1-234 <IT0>
A:Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R:Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahata, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1986
A>Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A:Reference number: A25451; MUID:86219712; PMID:3519138
A:Accession: A25451
A:Molecule type: DNA
A:Residues: 1-234 <IIt2>
A>Note: This sequence differs from that shown in having a Gln inserted between residues
R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A>Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF
A:Reference number: JH0309; MUID:91065534; PMID:2249779
A:Accession: JS0727
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62,'Q','G3'-234 <SHA>
A:Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
C:Genetics:
A:Introns: 62/3; 80/1; 96/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxic; glycoprotein; lipoprotein; lymphokine; macrophage; mem
E:1-81/Domain: propeptide #status predicted <PRO>
F:82-234/Product: tumor necrosis factor #status predicted <MAT>
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:83/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:147-178/Disulfide bonds: #status predicted

```
Query Match          9.5%; Score 141; DB 1; Length 234;
Best Local Similarity 22.4%; Pred.No. 0.00016;
Matches    62; Conservative   41; Mismatches     98; Indels      76; Gaps       13;
```

Qy 8 GGPSLGTCVLIVFTVLLQSCLVAITYVFTELKQMOKYSGKIACFLKEDDSYWDP 67
||| : | : | : ||
Db 22 GGFGSRRGLSLSEELL-----VAGATTTF-----CLL--HFRVIGP 58
||| : | : | : ||

Qy 68 NDRESMNSPCWKQLRLVRKMI-LRTSEETISTVEKKQNISPLVRERGPORVAHI 126
:||| : | : | : ||
Db 59 QEBESPNN-----LHLVPFAQVTLSRASALSD-----KPL-----AHV 94
||| : | : | : ||

Qy 127 TGTRGRNTLUSSPNKNKEALGRKINSWSRSRGSHSFNLHLNGELVTHEKGFIYYIS 186
:||| : | : | : ||
Db 95 VA-----NPQVEQQ-----OWLSQRANALLANGMKLTDLVVFPADGLYLIYS 138
||| : | : | : ||

Qy 187 QTVRFQEIKENTKNDKWQVIYTK-TSPDPIILAKMSARNSCWSKDAEYG----LY 240
:||| : | : | : ||
Db 139 QVLFSGQ-----GCRSVLVITHVSRAFYPPNKVNILLSAIKSPCHRETPEEAPMAWE 193
:||| : | : | : ||

Qy 241 SIYGGIFELKENDRIFFSVTNEHLIMDHAS-FFG 276
:||| : | : | : ||
Db 194 PIYLGVFOLEKGBRELSTEVNQPEYLDLAESGOVYFG 230
:||| : | : | : ||

```

A;Residues: 1-260 <ARM>
A;Cross-references: EMBL:X65453; NID:G50351; PIDN:CAA46448.1; PID:G50352
C;Keywords: glycoprotein; transmembrane protein
F;23-46/Domain: transmembrane #status predicted <TM>
F;47-260/Domain: extracellular #status predicted <EXT>
F;239/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          9.5%; Score 141; DB 2; Length 260;
Best Local Similarity 23.5%; Pred. No. 0.00019;
Matches 59; Conservative 50; Mismatches 104; Indels 38; Gaps 11;

QY 17 VLIVIEFVLV--QSLVAVVYVFTNELKQMDQKYSKSGIACELKEDSDSYWDNDESMN 74
Db 23 IFWLLVFLITQMIGVLFAYLHRRDKVVEEVLHEDFVFKLKRC---NKGGSL 79
QY 75 S--PCWQVKQLRQLVRKMLRTSEETISTVQEKQNNISPLVRERGQRVAAHITGTRGR 132
Db 80 SLLNCEEMRQFEDLVKIDITLNK-----EEKKNSFEMQGDDEPQIAAHV----- 125
QY 133 SNTLSSPNSKNEKALGRKINSWSSRSRSGHSLNL-HLRNG-ELVIEKGFYIYQTYF 190
Db 126 ---VSEANSAAVSL-----QW-AKGYITMKSNLVLENGKQITVREGLYIYVYQVTF 176
QY 191 RFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLYSIYQGGIFEL 250
Db 177 CSNRE----PSSQRPFFVGLWLPKFSIGSERILLKAAANTHSSSQCEQ--QSVHLGGVFEL 230
QY 251 KENDRIFSVVT 261
Db 231 QAGASVFVNVT 241

RESULT 8
S17289
tumor necrosis factor beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S17289
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A;Reference number: S17289; MUID:91340150; PMID:1874444
A;Accession: S17289
A;Molecule type: DNA
A;Residues: 1-204 <KH>
A;Cross-references: EMBL:X54859; NID:G2132; PIDN:CAA38638.1; PID:G2133
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match          9.1%; Score 134.5; DB 1; Length 204;
Best Local Similarity 24.7%; Pred. No. 0.00048;
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;

QY 101 STVQEKQNTISPLVRERGQRVAAHITG-----TRGRNTLSSPNSKNEKALGRKINS 153
Db 42 SAAQPAHQH-PPKHLAGTGLKPAHLVGDPESTPDLEWRANT-----DRAFLR---- 88
QY 154 WESSRSRSGHSLNLHANGELVIEKGFYIYQTYFRFQEEIKENTKNDKQMVQYIYKY 213
Db 89 -----HGEL----LNSNLLVPTSGLYFVSQVFSFGCGPPKATPTPLYLAHEVQLF 137
QY 214 TS-YPDILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFSVTNEHLIDMDHEA 272
Db 138 SSQYFFHVPVLLSAQKSVCPGPGPW-VRSVYQGAVELLTQGDQLSTHDTGTPHLLSPSS 196
QY 273 SFFGAF 278
Db 197 VFFGAF 202

```

RESULT 9

```

S12606
tumor necrosis factor alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: S12606; S17290; S18965; I46659
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis factor alpha.
A;Reference number: S12606; MUID:91016861; PMID:2216741
A;Accession: S12606
A;Molecule type: DNA
A;Residues: 1-232 <DRE>
A;Cross-references: EMBL:X54001; NID:G2135; PIDN:CAA37949.1; PID:G2136
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative ana
A;Reference number: S17289; MUID:91340150; PMID:1874444
A;Accession: S17290
A;Molecule type: DNA
A;Residues: 1-232 <KH>
A;Cross-references: EMBL:X54859; NID:G2132; PIDN:CAA38639.1; PID:G2134
A;Note: the authors translated the codon GAG for residue 202 as Gly
R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis f
A;Reference number: S18965
A;Accession: S18965
A;Molecule type: mRNA
A;Residues: 1-232 <CHO>
A;Cross-references: EMBL:X57321; NID:G2137; PIDN:CAA40591.1; PID:G2138
R;Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reactic
A;Reference number: I46659; MUID:90034181; PMID:2478420
A;Accession: I46659
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
A;Cross-references: GB:M29079; NID:G164694; PIDN:AAA31128.1; PID:G164695
C;Genetics:
A;Introns: 62/3; 78/1; 93/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myr
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted

Query Match          9.0%; Score 133; DB 1; Length 232;
Best Local Similarity 21.3%; Pred. No. 0.00076;
Matches 61; Conservative 40; Mismatches 100; Indels 86; Gaps 11;

QY 2 AMMEVQGGPSLQGTQVLIVIFVILQSLCVATYVYFTNELKQMDQKYSKSGIACFLKED 61
Db 16 ALAKKAGGPGGRRRCCLCSLFSFLL-----VAGATTFL-----CLLHFE 54
QY 62 DSYWDNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNTISPLVRERGQR 121
Db 55 --VIGPQKEFPAGPL-----SINPLAQ----- 75
QY 122 VAAHTGTGRNTLSSPNS---KNEKALGRKINSWSSRSRSGHSLNLHANGELVIEH 178
Db 76 -----GLASSQTSKPKVAHVAVNKAEGQL--QWQSGYANALLANGVKLKDNLVVP 127
QY 179 KGFYIYQTYFRFQEEIKEN---TWQDKQMVQYIYKYTSYDPDILLMKSARNSCWSK-- 233
Db 128 DGLYLIYSQVLPFGQCGCPSTNVFLTHTSRIA-----VSYQTKVNLLSAIKSPQORETP 181
QY 234 ---DARYGLYSIQGGIFELKENDRIFSVTNEHLIDMDHEAS-PFG 276

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Db 182 EGAEAKPWEPYILGGVQLEKDDRLSAEINLPDYLDFAESGGVYFG 228

RESULT 10

S22052

tumor necrosis factor alpha precursor - baboon

C;Species: Papio sp. (baboon)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C;Accession: S22052

R;Sanjwal, M.; Edwards, A.

submitted to the EMBL Data Library, September 1991

A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A;Reference number: S22052

A;Accession: S22052

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-233 <SAN>

A;Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160

C;Genetics:

A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;19/20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 8.9%; Score 131.5; DB 1; Length 233;

Best Local Similarity 19.2%; Pred. No. 0.001;

Matches 55; Conservative 49; Mismatches 98; Indels 85; Gaps 10;

QY 2 AMNEVGQPSLGGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKGIACFLKED 61

Db 16 ALPKYGGPGSRCLLSLFSLLVAGATLCLLHFGVIGPQREFFPK----- 65

QY 62 DSYWDPNDESMNSPCQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRGPOR 121

Db 66 ----DP-----SLISPLAQA-----VRSSRTPS-----DK 87

QY 122 VAHITGRGSRNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKGF 181

Db 88 PVAHVVA-----NPQAEGL--QWLNRANALLANGVELRDNLQVLPVSEGL 131

QY 182 YTYISQTYFRFQEEIKENTKNDKQMVQYIVKYT-----SYDPDILLMKSARNCSWSK-- 233

Db 132 YLYISQVLFKQ-----GCPSTHLLTHTSRLAVSYPSKVNLLSAIKSPCHTE 181

QY 234 ----DAEYGLSYIYOGGIFELKENDRIFVSVTNEHLIDMDHEAS--FFG 276

Db 183 EGAEAKPWEPYILGGVQLEKDDRLSAEINLPDYLDFAESGGVYFG 229

RESULT 11

QJ1344

tumor necrosis factor alpha precursor - horse

N;Alternate names: cachectin; TNF alpha

C;Species: Equus caballus (domestic horse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C;Accession: JQ1344

R;Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis

A;Reference number: JQ1344; MUID:92084125; PMID:1748301

A;Accession: JQ1344

A;Molecule type: DNA

A;Residues: 1-234 <SUX>

A;Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245

C;Comment: This protein is an important proximal mediator of endotoxemia.

C;Genetics:

A;Introns: 62/3; 79/1; 95/1

C;Superfamily: tumor necrosis factor

C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb

F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F;19/20/Binding site: myristate (Lys) (covalent) #status predicted

F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;146-178/Disulfide bonds: #status predicted

Query Match 8.9%; Score 131; DB 1; Length 234;

Best Local Similarity 20.8%; Pred. No. 0.0011;

Matches 60; Conservative 40; Mismatches 89; Indels 100; Gaps 13;

QY 8 GGPGLGOTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKGIACFL-----K 59

Db 22 GGPQGRCLCLSLFSLFLL-----VAGATTLF-----CULHFGVIGPQR 60

QY 60 EDSYWDPNDESMNSPCQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRGP 119

Db 61 EEQL-----PNAFQIN-PLAQT-----LRSSRTPS----- 86

QY 120 ORVAHITGRGSRNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEK 179

Db 87 DKPVAHVVA-----NPQAEGL--QWLNRANALLANGVELRDNLQVLPD 130

QY 180 GFYIYSQTYFRFQEEIKENTKNDKQMVQYIVKYT-----SYDPDILLMKSARNCSWSK 233

Db 131 GLYLYISQVLFKQ-----GCPSTHLLTHTSRLAVSYPSKVNLLSAIKSPCHTE 181

QY 234 DAEYG-----LYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEAS--FFG 276

Db 182 SPEQAEAKPWEPYILGGVQLEKDDRLSAEINLPDYLDFAESGGVYFG 230

RESULT 12

S24642

tumor necrosis factor alpha precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C;Accession: I46047; S24642

R;Cluets, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and

A;Reference number: I46046; MUID:94083525; PMID:8260599

A;Accession: I46047

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-233 <CL2>

A;Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C;Genetics:

A;Gene: TNFA

A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 8.8%; Score 130.5; DB 1; Length 233;

Best Local Similarity 20.3%; Pred. No. 0.0013;

Matches 59; Conservative 43; Mismatches 95; Indels 93; Gaps 13;

QY 3 MMEVQGPSLGGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKGIACFL---- 58

Db 17 LSEKAGGPGSRCLCLSLFSLFLL-----VAGATTLF-----CULHFGV 55

QY 59 ----KEDDSYWDPNDESMNSPCQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVR 115

Db 56 IGQREESPGGP-----SINSLVQT-----LRSSQASS----- 85

QY 116 ERGPORVAHITGRGSRNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV 175

Db 86 ----NKPVAHVVA-----DINSPQLR-----WSDSYANALMANGVKLEDNLV 125

QY 176 IHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYK--YTSDPDILLMKSARNSC-- 230

Db 126 VPADGLYLYISQVLFKQ-----GCPSTPLFLTHTSRLAVSYQTKVNLLSAIKSPCHRE 180

A:Cross-references: GB:M26331; NID:G339763; PIDN:AAA36758.1; PID:G339764
 A:Experimental source: U-937 cells
 R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
 Eur. J. Biochem. 235, 431-437, 1996
 A:Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
 A:Reference number: S62610; MUID:96202967; PMID:8631363
 A:Accession: S62610
 A:Molecule type: protein
 A:Residues: 77-99 <TAK>
 R:D'Alfonso, S.; Richiardi, P.M.
 Immunogenetics 39, 150-154, 1994
 A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter region
 A:Reference number: I54522; MUID:94102809; PMID:7903959
 A:Accession: I54522
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-8 <DAL>
 A:Cross-references: GB:S68530; NID:G544751
 R:Stevenson, F.T.; Hursten, S.L.; Locksley, R.M.; Lovett, D.H.
 J. Exp. Med. 176, 1053-1062, 1992
 A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys
 A:Reference number: A59163; MUID:93018820; PMID:1402651
 A:Contents: annotation; identification of myristylated lysines
 R:Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Brin
 J. Biol. Chem. 260, 2345-2354, 1985
 A:Title: Human tumor necrosis factor. Production, purification, and characterization.
 A:Reference number: A92511; MUID:85130974; PMID:3871770
 A:Contents: annotation; disulfide bond
 C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction
 out detriment to normal cells. It can also act synergistically with interferon gamma to
 C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely
 ut are produced by different cell types and have different induction kinetics.
 C:Genetics:
 A:Gene: GDB:TNF; TNFA
 A:Cross-references: GDB:120441; OMIM:191160
 A:Map position: 6p21.3-6p21.3
 A:Introns: 62/3; 78/1; 94/1
 C:Complex: homotrimer
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macr
 F:1-76/Domain: propeptide #status predicted <PRO>
 F:77-233/Product: tumor necrosis factor #status experimental <NAT>
 F:19,20/Binding site: myristate (Lys) (covalent) #status experimental
 F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
 F:145-177/Disulfide bonds: #status experimental

Query Match 8.5%; Score 125.5; DB 1; Length 233;
 Best Local Similarity 17.8%; Pred. No. 0.0033;
 Matches 51; Conservative 52; Mismatches 99; Indels 85; Gaps 9;

QY	2	AMMEVGGPSLQTCVLIVIFVILLOSCLVAVTVYVFNELKQMDKYSKGIACFLKED 61
Db	16	ALPKTTGGPQGRRCFLFLSLFSLVAGATTLFLLHFGVIGVQREFFPR----- 65
QY	62	DSYWDPNDESMNSPCQVQKWQLQVIRKMLIRTSBETISTVQEQQNISPLVRERGPR 121
Db	66	-----DLSLISPLAQ-----VRSSRTPS-----DK 87
QY	122	VAAHTTGRNRTLSSPNSKNEKALGRKINKSWESRSHSFLSNLHNGELVIEKGF 181
Db	88	PVAHVVA-----NPAEGQL--QWLNRANALLANGVELRDNLVVPSEGL 131
QY	182	YVIYSQTYRFFQEEIKENTKDKQVQYIYKYT-----SYDDPILLMKASNSCWSK-- 233
Db	132	YLIYSQVLFPKGQ-----GCPSTHLLTHTTISRIAVSYQTKVNLLSAIKSPQRETP 182
QY	234	---DAEYGLIYSYQGGIFELKENDRFVSVTNEHLIDMDHEAS-RFG 276
Db	183	EGAEAKPWTEPIYLGGVFQLEKGRUSAEINRPDYLDFAESGVVYFG 229

Search completed: March 23, 2004, 09:07:19
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:04:03 ; Search time 17 Seconds
(without alignments)

860.689 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMEVQGGPSLQGTCTLV.....NEHLIDMDHEASPFGLV 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	1	TN10 HUMAN
2	930	62.9	231	1	TN10 MOUSE
3	267.5	18.1	318	1	TN11 RAT
4	258.5	17.5	316	1	TN11 MOUSE
5	251.5	17.0	317	1	TN11 HUMAN
6	189.5	12.8	279	1	TNF6 MOUSE
7	187	12.7	280	1	TNF6 CERTO
8	185	12.6	281	1	TNF6 HUMAN
9	185	12.5	280	1	TNF6 MACMU
10	184	12.4	272	1	TNF5 CHICK
11	182	12.3	282	1	TNF6 PIG
12	177.5	12.0	278	1	TNF6 RAT
13	164	11.1	261	1	TNF5 BOVIN
14	160	10.8	174	1	TN15 HUMAN
15	159.5	10.8	240	1	TN14 HUMAN
16	152.5	10.3	239	1	TN14 MOUSE
17	152	10.3	261	1	TNF5 CALJA
18	150.5	10.2	261	1	TNF5 AOTTR
19	149.5	10.1	260	1	TNF5 FELCA
20	148	10.0	261	1	TNF5 MACMU
21	147.5	10.0	260	1	TNF5 CANFA
22	147.5	10.0	261	1	TNF5 HUMAN
23	143	9.7	261	1	TNF5 PIG
24	140	9.5	260	1	TNF5 MOUSE
25	136.5	9.2	235	1	TNFA RABIT
26	135	9.1	229	1	TNFB CEREL
27	134.5	9.1	204	1	TNFB PIG
28	134	9.1	234	1	TNFA BOSIN
29	133.5	9.0	260	1	TNF5 RAT
30	133	9.0	232	1	TNFA PIG
31	133	9.0	234	1	TNFA CAVPO
32	131.5	8.9	233	1	TNFA BUBBU
33	131.5	8.9	233	1	TNFA PAPSP

RESULT 1					
TN10 HUMAN					
ID	TN10 HUMAN	STANDARD;	PRT;	281 AA.	
AC	P50531;				P29553 equus cabal
DT	01-OCT-1996 (Rel. 34, Created)				O8jfg3 sparus aura
DT	01-OCT-1996 (Rel. 34, Last sequence update)				Q06599 bos taurus
DT	10-OCT-2003 (Rel. 42, Last annotation update)				P36939 peromyscus
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related				Q06600 bos taurus
DE	apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).				O35734 marmota mon
GN	TNFSF10 OR TRAIL OR APO2L.				P01375 homo sapien
OS	Homo sapiens (Human)				P06804 mus musculus
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				P16599 rattus norv
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				P01374 homo sapien
OX	NCBI_TaxID=9606;				Q8hd9 pan troglod
[1]					P13296 capra hircu
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96111955; PubMed=8777713;				
RA	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,				
RA	Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,				
RA	Goodwin R.G.;				
RT	"Identification and characterization of a new member of the TNF				
RL	family that induces apoptosis."				
RL	Immunity 3:673-682(1995).				
[2]					
RN	SEQUENCE FROM N.A.				
RP	TISSUE=Placenta;				
RC	MEDLINE=96278649; PubMed=86631110;				
RX	Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,				
RA	Ashkenazi A.;				
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor				
RT	necrosis factor cytokine family."				
RL	J. Biol. Chem. 271:12687-12690(1996).				
[3]					
RN	SEQUENCE FROM N.A.				
RP	TISSUE=Lymph;				
RC	MEDLINE=23388257; PubMed=12477932;				
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalus D.E.,				
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,				
RT	"Generation and initial analysis of more than 15,000 full-length				
RT	human and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				

ALIGNMENTS

[4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 RX MEDLINE=20017054; PubMed=10542988;
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 RT complex with death receptor 5";
 RL Mol. Cell 4:563-571(1999).
 [5]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 RP PubMed=10542098;
 RX Mongkoleapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Sreaton G.R.;
 RA "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 RT specificity in apoptotic initiation";
 RL Nat. Struct. Biol. 6:1048-1053(1999).
 [6]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 RX MEDLINE=99413670; PubMed=10485660;
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
 RA Sung Y.C., Oh B.-H.;
 RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with
 RT selective antitumor activity";
 RL Immunity 11:253-261(1999).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 CC -1- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 CC trimer.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
 CC AND PROSTATE.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC
 DR EMBL; U37518; AAC50332.1; -;
 DR EMBL; U57059; BAB01233.1; -;
 DR EMBL; BC032722; AAH32722.1; -;
 DR PDB; 1D0G; 22-OCT-99.
 DR PDB; 1D4V; 01-NOV-99.
 DR PDB; 1D2Q; 11-FEB-00.
 DR PDB; 1DG6; 26-SEP-01.
 DR Gnew; HGNC:11925; TNFRSF10.
 DR MM; 603598; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005102; F:receptor binding; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0006917; P:induction of apoptosis; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF-like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00499; TNF_2; 1.
 KW Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
 KW Zinc; 3D-structure.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT DOMAIN 39 281 (POTENTIAL).
 FT METAL 230 127 EXTRACELLULAR (POTENTIAL).
 FT STRAND 123 131 ZINC.
 FT TURN 130 131
 FT TURN 137 139
 FT STRAND 149 150
 FT STRAND 163 165
 FT STRAND 167 170
 FT TURN 171 172
 FT STRAND 173 176
 FT STRAND 180 193
 FT STRAND 205 213
 FT STRAND 220 228
 FT STRAND 237 250
 FT TURN 252 253
 FT STRAND 255 260
 FT HELIX 263 265
 FT STRAND 266 267
 FT TURN 270 272
 FT STRAND 274 281
 SQ SEQUENCE 281 AA; 32509 MW; DDAAF78DAAB2F6D CRC64;
 Query Match 100.0%; Score 1478; DB 1; Length 281;
 Best Local Similarity 100.0%; Pred No. 8e-115;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMVEQGQPSLGQTCVLIVFTVLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMVEQGQPSLGQTCVLIVFTVLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
 QY 61 DSYWDPNDEESMNSPCWQKQVLVKMLRTSEETISTVQEQQNISPLVREGPQ 120
 DB 61 DSYWDPNDEESMNSPCWQKQVLVKMLRTSEETISTVQEQQNISPLVREGPQ 120
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKG 180
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKG 180
 QY 181 FYYISQTYFRQEEIKENTKNDKQVYIYKYTSYPPDILLKMSARNSCKDAEYGLY 240
 DB 181 FYYISQTYFRQEEIKENTKNDKQVYIYKYTSYPPDILLKMSARNSCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 RESULT 2
 TN10_MOUSE STANDARD; PRT; 291 AA.
 ID TN10_MOUSE
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9611955; PubMed=8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT Identification and characterization of a new member of the TNF
 RT family that induces apoptosis";
 RL Immunity 3:673-682(1995).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and

RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RL Cell 76:969-976(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6; PubMed=7544870;
RX MEDLINE=95388076; PubMed=7544870;
RA Peitsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family";
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster.";
RL Immunity 1:131-136(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX STRAIN=BALB/c;
RA Fennel M.H., Shioda T., Isselbacher K.J.;
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT two amino acids.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX STRAIN=C3H; TISSUE=Spleen;
RA Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,
RA Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
RT "Cloning and expression of a short Fas ligand: A new alternatively
RT spliced product of the mouse Fas ligand gene.";
RL Blood 94:3456-3467(1999).
RN [6]
RP CHARACTERIZATION OF VARIANT GLD.
RX MEDLINE=96091792; PubMed=7495745;
RA Hahne M., Peitsch M.C., Imler M., Schroeter M., Lowin B.,
RA Rausseau M., Bron C., Renno T., French L., Tschopp J.;
RT "Characterization of the non-functional Fas ligand of gld mice.";
RL Int. Immunol. 7:1381-1386(1995).
RN [7]
RP VARIANTS ALA-184 AND GLY-218.
RX STRAIN=C57BL/6, C3H, MRL, SJL, NOD, NZB, NZW, BALB/c, DBA/1, and
RA DBA/2;
RX MEDLINE=97268671; PubMed=9108079;
RA Kiyagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,
RA Yagita H.;
RT "Polymorphism of murine Fas ligand that affects the biological
RT activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).
RN [8]
RP FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
RX transduces the apoptotic signal into cells. May be involved in
RA cytotoxic T cell mediated apoptosis and in T cell development.
RX TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
RA peripheral tolerance, in the antigen-stimulated suicide of mature
RA T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
RA modulates its effects (By similarity).
RX [SUBUNIT: Homotrimer (Probable).]
RX [SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
RX Secreted (isoforms FASL and FASLS).]
RN [9]
RP ALTERNATIVE PRODUCTS:
RX Event=Alternative splicing; Named isoforms=2;
RA Name=FasL;
RX IsoId=P41047-1; Sequence=Displayed;
RA Name=FasLS;
RX IsoId=P41047-2; Sequence=VSP_006445;
RA [PTM: The soluble form derives from the membrane form by
RA proteolytic processing (By similarity).]
RN [10]
RP DISEASE: A deficiency in this protein is the cause of generalized

CC lymphoproliferation disease phenotype (gld). Gld mice present
CC lymphadenopathy and autoantibody production. The phenotype is
CC recessively inherited.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC EMBL; U06948; AAA17800.1; -
CC EMBL; U10984; AAA19778.1; -
CC EMBL; S76752; AAB33780.1; -
CC EMBL; U58985; AAB02915.1; -
CC EMBL; AF119335; AAD52106.1; -
CC PIR; A53062; A53062.
CC HSSP; P01375; 4TSV.
CC MGD; MGI:99255; Tnfsf6.
CC InterPro; IPR008064; Fas ligand.
CC InterPro; IPR006053; TNF_abc
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01681; FASLIGAND.
CC PRODOM; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS00449; TNF 2; 1.
CC KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
CC Disease mutation; Polymorphism; Alternative splicing;
CC FT CHAIN 1 279 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC FT CHAIN 128 279 MEMBER 6, MEMBRANE FORM.
CC FT CHAIN 128 279 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC FT DOMAIN 1 78 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
CC FT TRANSMEM 79 100 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 101 279 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT DOMAIN 4 69 (POTENTIAL).
CC FT DOMAIN 45 51 EXTRACELLULAR (POTENTIAL).
CC FT SITE 127 128 PRO-RICH.
CC FT SITE 127 128 POLY-PRO.
CC FT DISULFID 200 231 CLEAVAGE (BY SIMILARITY).
CC FT CARBOHYD 117 117 POTENTIAL.
CC FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARSPLIC 1 210 Missing (in isoform FASLS).
CC FT /FTId=VSP_006445.
CC FT VARIANT 184 184 T -> A (IN STRAINS BALB/C AND DBA;
CC FT ENHANCES CYTOTOXICITY).
CC FT VARIANT 218 218 E -> G (IN STRAINS BALB/C AND DBA;
CC FT ENHANCES CYTOTOXICITY).
CC FT VARIANT 273 273 F -> L (IN GLD; ABOLISHES BINDING OF FASL
CC FT TO ITS RECEPTOR).
CC SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;
CC
CC Query Match 12.8%; Score 189.5; DB 1; Length 279;
CC Best Local Similarity 25.8%; Pred. No. 1.9e-08;
CC Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;
CC
CC QY 83 QLRQLVRKMLTSETSTVQEKQNTISPLVRGPGQVAAHITGRSNTLSPNSK 142
CC Db 111 ELREFTNQSL-----KVSSFEKQIANPSTPSEKPRSV-AHLTG-----NPHSR 154
CC QY 143 NKKALGRKINSWESSRSGHSFLSNLHNGELVIHEKGFYIYSQTYFRFQBEIKENTGN 202
CC Db 155 SIPL-----EWEDT-YGTALISGVKYKGLVINETGLYFYVSKYFRGQ-----SCN 201

QY 203 DKOMQVYIY-KYTSYDPDILLMKSR-NSCWSKDAEYGLYSIYGGIFELKENDRIFVSU 260
 Db 202 NQPLNKHVNRNSKYEDLVIMBEKRLNYCTT--GQIWAHSYLGAVENLTSDADHLYVNI 259
 QY 261 TNEHLIDMDHEASFFGAF 278
 Db 260 SQLSLINFESKTFGLY 277

RESULT 7
 TNF6_CERTO STANDARD; PRT; 280 AA.
 AC Q9BDN1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
 DE (CD95L protein).
 GN TNFSF6 OR FASL OR CD95L.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopitheciinae; Cercopithecus.
 OC NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/FasL ligand and co-stimulatory molecules";
 RL Immunogenetics 53:315-328(2001).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
 CC modulates its effects (By similarity).
 CC -!- SUBUNIT: Homotrimer (Probable).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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 CC -----
 DR EMBL; AF348487; AAK37606.1; -
 DR HSSP; P01375; 4TSV.
 DR InterPro; IPR008064; Fas ligand.
 DR InterPro; IPR006053; TNF_abc.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01681; FASLIGAND.
 DR PRINTS; PR01234; TNFROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF; 1.
 DR PROSITE; PS00049; TNF; 2; 1.
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY.
 FT MEMBER 6, MEMBRANE FORM.
 FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

FT DOMAIN 1 80 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
 FT TRANSMEM 81 101 CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT PRO-RICH.
 FT POLY-PRO.
 FT CLEAVAGE (BY SIMILARITY).
 FT SITE 128 129 POTENTIAL.
 FT DISULFID 201 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;
 Query Match 12.7%; Score 187; DB 1; Length 280;
 Best Local Similarity 22.1%; Pred. No. 3e-08;
 Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;
 QY 4 MEVQGPSLGQTCVLIVITVLQSLCVAVTVVYFTNELKOMQDKYSKGIACELKEDDS 63
 Db 70 LKKRGHSTG-ICLLVFMFVNLVALVGLGFMQLFHLOKELAE-----LRETS 118
 QY 64 YWDPNDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNMISPLVRERGQRYA 123
 Db 119 -----QKHTASSLEKQIGHPS-PPEKKEQKV 145
 QY 124 AHITGRGRSVTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKGFY 183
 Db 146 AHLTG-----KPSRSMP-----EWEDT-YGIVLLSGVYKKGGLVINETGLYF 189
 QY 184 IYSQTVRFOEBIKENTKNDKQMVQYIY-KYTSYDPDILLMKSRNSCWSKDAEYGLYSI 242
 Db 190 VISKVYFRQ-----SCNLPFSHKVYMRNSKYQDVLVMEGKAMS-YCTTGQMWAHSS 242
 QY 243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 Db 243 YLGAVENLTSTDHLYVNVSELSLVNFERSQTFGLY 278

RESULT 8
 TNF6_HUMAN STANDARD; PRT; 281 AA.
 ID TNF6_HUMAN
 AC P48023; Q9BZP9;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
 DE (Apoptosis antigen ligand) (APTL) (CD178 antigen).
 GN TNFSF6 OR FASL OR APTLGL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=95105731; PubMed=7528780;
 RA Alderson M.;
 RT "Fas ligand mediates activation-induced cell death in human T
 RT lymphocytes";
 RL J. Exp. Med. 181:71-77(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=95127560; PubMed=7826947;
 RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
 RT "Human Fas ligand: gene structure, chromosomal location and species
 RT specificity";
 RL Int. Immunol. 6:1567-1574(1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Schaeuble C.E., Poehmann R., Philippsen P., Eibel H.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).


```

RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,
RT Fusamoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT infection.";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT "Isolation and characterization of a new naturally occurring variant of
RT human Fas ligand that is expressed only in membrane bound form.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBSJ databases.
RN [6]
RN SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBSJ databases.
RN [7]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RN SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBSJ databases.
RN [9]
RX CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
RA MEDLINE=97373583; PubMed=9228058;
RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Sauteri P.,
RA Terakih A., Peitsch M.C., Tschopp J.;
RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
RL J. Biol. Chem. 272:18827-18833(1997).
RN [10]
RN PROCESSING.
RX MEDLINE=98087475; PubMed=9427603;
RA Tanaka M., Itai T., Adachi M., Nagata S.;
RT "Downregulation of Fas ligand by shedding.";
RL Nat. Med. 4:31-36(1998).
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
CC modulates its effects.
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released
CC into the extracellular fluid, probably by cleavage from the cell
CC surface.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;

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CC CC IsoId=P48023-1; Sequence=Displayed;
CC CC Name=2;
CC CC IsoId=P48023-2; Sequence=VSP_006443, VSP_006444;
CC CC -!- PTM: N-glycosylated.
CC CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing.
CC CC -!- DISEASE: Defects in TNFSF6 are a cause of autoimmune
CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
CC involving hemolytic anemia and thrombocytopenia with massive
CC lymphadenopathy and splenomegaly.
CC CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
CC CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674.g.htm".
CC CC
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CC or send an email to license@isb-sib.ch).
CC CC
CC EMBL; X89102; CAA61474.1; -
CC EMBL; U08137; AAC50071.1; -
CC EMBL; U11821; AAC50124.1; -
CC EMBL; D38122; BAA07320.1; -
CC EMBL; AF288573; AAG60017.1; -
CC EMBL; Z96050; CAB09424.1; -
CC EMBL; BC017502; AAI17502.1; -
CC EMBL; AB013303; BAA32542.1; -
CC PIR; I38707; I38707.
CC HSSP; P01375; 1TNF.
CC Genew; HGNC:11936; TNFSF6.
CC MIM; 134638; -
CC MIM; 601859; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005102; F: receptor binding; TAS.
CC GO; GO:0007267; P: cell-cell signaling; TAS.
CC GO; GO:0006917; P: induction of apoptosis; TAS.
CC GO; GO:0007145; P: signal transduction; TAS.
CC InterPro; IPR008064; Fas_ligand.
CC InterPro; IPR006053; TNF_abc.
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01681; FASLIGAND.
CC PRINTS; PR01234; TNFROSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS00049; TNF_2; 1.
CC Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
CC Alternative splicing; Antigen.
CC CHAIN 1 281
CC CHAIN 130 281
CC CHAIN 1 80
CC CHAIN 81 102
CC DOMAIN 103 281
CC DOMAIN 4 70
CC DOMAIN 45 65
CC SITE 129 130
CC DISULFID 202 233
CC CARBOHYD 184 184
CC CARBOHYD 250 250
CC CARBOHYD 260 260
CC VARSPPLIC 117 127
CC FT FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC FT FT MEMBER 6, MEMBRANE FORM.
CC FT FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC FT FT MEMBER 6, SOLUBLE FORM.
CC FT FT CYTOPLASMIC (POTENTIAL)
CC FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT FT (POTENTIAL).
CC FT FT EXTRACELLULAR (POTENTIAL).
CC FT FT PRO-RICH.
CC FT FT POLY-PRO.
CC FT FT CLEAVAGE.
CC FT FT POTENTIAL.
CC FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT FT STSQMHTASSL -> ATPVHPLKRS (in isoform
CC FT FT 2)
CC FT FT /FTId=VSP_006443.

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CC CC -!- SUBUNIT: Homotrimer (Potential).  
CC CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
CC CC similarity).  
CC CC -!- PTM: The soluble form derives from the membrane form by  
CC CC proteolytic processing (By similarity).  
CC CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
-----  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to license@isb-sib.ch).  
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EMBL; AF344856; AAK37539.1; -;  
DR DDB AB035138; BAA90294.1; -;  
CC EMML; AB035139; BAA90295.1; -;  
DR DDB EMBL; AB035140; BAA90296.1; -;  
CC HSSP; P01375; 4TSV.  
DR InterPro; IPR008064; Fas ligand.  
DR InterPro; IPR006053; TNF abc.  
DR InterPro; IPR006052; TNF family.  
DR InterPro; IPR008983; TNF like.  
DR InterPro; IPR003636; TNF_subf.  
CC Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01681; FASLGAND.  
DR PRINTS; PR01234; TNECROSISPTCT.  
DR ProDom; PD002012; TNF_subfi; 1.  
DR SMART; SMO0207; TNF; 1.  
DR PROSITE; PS00251; TNF 1; 1.  
DR PROSITE; PS00049; TNF 2; 1.  
CK Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.  
FT FT CHAIN 1 280 TUMOR NECROSI FACTOR LIGAND SUPERFAMILY  
FF FF MEMBER 6, MEMBRANE FORM.  
FT FT CHAIN 129 280 TUMOR NECROSI FACTOR LIGAND SUPERFAMILY  
FF FF DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).  
FT FT TRANSMEM 81 101 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FF FF (POTENTIAL).  
FF FF DOMAIN 102 280 EXTRACELLULAR (POTENTIAL) .  
FF FF DOMAIN 4 69 PRO-RICH.  
FF FF DOMAIN 45 64 POLY-PHO.  
FF SITE 128 129 CLEAVAGE (BY SIMILARITY) .  
FF DISULFD 201 232 POTENTIAL.  
FF CARBOHYD 183 183 N-LINKED (GLCNAC.. ) (POTENTIAL) .  
FF CARBOHYD 249 249 N-LINKED (GLCNAC.. ) (POTENTIAL) .  
FF CARBOHYD 259 259 N-LINKED (GLCNAC.. ) (POTENTIAL) .  
FF CONFLICT 60 60 S --> P (IN REF. 1).  
SQ SEQUENCE 280 AA; 31367 MW; FOB2B4DD61A132EB4 CRC64;  
  
Query Match 12.5%; Score 185; DB 1; Length 280;  
Best Local Similarity 22.1%; Pred. No. 4.4e-08;  
Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;  
  
QOY 4 MEVGGPSLSGQTCLVLIVITFLQLSLCAVVTVVFYNELKQMODYSKSGIACFLKEDDS 63  
::|||:|||::|||::|||::|||::|||::|||:  
Db 70 LKKRGNHSTGT-LCLLVMPFMWVALVGLGLGFOLFHLQKLAE -----LRSTS 118  
64 YWDPNDEESMNPCPVQVKWLRLVRKMILRTFSSETISTVSQEQKNISPLVERGPQRVA 123  
::|||::|||::|||::|||::|||::|||:  
Db 119 -----OKHTASLESKIQHPSPEKEQRKV 145  
124 AHITTGRGSNTLSPNSNKNEALKRKINSWESSRSCHSFSLNHLRNGLVELTHEKGFY 183  
::|||::|||::|||::|||::|||::|||:  
Db 146 AHLTG-----KPNSRMPL-----EWEDT-YGVILLGGVKKYGGLVINETGLYF 189  
184 YYSQTYFRFOBEIKENTKDGMQVIYY-KYTYSYDPDLLMKSAARNCSWKDAEYLGI 242  
::|||::|||::|||::|||::|||::|||:  
Db 190 VYSKYVIFRGQ-----SCTNLFSLSHKVMRKSNPKPDLLMMEGRWMS-YCTTTGMWAHS 242  
243 YOGGFEFKENDRIEFVSVTNEHLIDMDHEASPFGAF 278  
::|||::|||::|||::|||::|||::|||:
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Db      243 YLGAVENTLSADHLYVNVSELSLVNEESQTFGLY 278
RESULT 10
TNF5_CHICK
ID      TNF5_CHICK  STANDARD;      PRT;      272 AA.
AC      Q91B58;
DT      28-FEB-2003 (Rel. 41, Created)
DT      15-MAR-2004 (Rel. 43, Last sequence update)
DE      Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
DE      L) (CD154 protein).
GN      TNFSF5 OR CD40LG OR CD40L.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=White leghorn; TISSUE=Spleen;
RA      Tregaskes C.A., Young J.R., Burnside J.;
RL      "Cloning of a putative chicken CD40 ligand.";
RL      Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC      proliferation in the absence of co-stimulus as well as IGE
CC      production in the presence of IL-4. Involved in immunoglobulin
CC      class switching (By similarity).
CC      -!- SUBUNIT: Homotrimer (By similarity).
CC      -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC      extracellular soluble form (By similarity).
CC      -!- PTM: The soluble form derives from the membrane form by
CC      proteolytic processing (By similarity).
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; AJ243435; CAB95748.2; --
CC      HSSP; P29965; ITALY
CC      GO; GO:0016021; C:integral to membrane; ISS.
CC      GO; GO:0005174; F:CD40 receptor binding; ISS.
CC      GO; GO:0042100; P:B-cell proliferation; ISS.
CC      GO; GO:0006954; P:inflammatory response; ISS.
CC      GO; GO:0007159; P:leukocyte cell adhesion; ISS.
CC      GO; GO:0030168; P:platelet activation; ISS.
CC      InterPro; IPR003263; TNF_5.
CC      InterPro; IPR006052; TNF family.
CC      InterPro; IPR008983; TNF like.
CC      InterPro; IPR003636; TNF_subf.
CC      Pfam; PF00229; TNF; 1.
CC      PRINTS; PR01702; CD40LIGAND.
CC      ProDom; PD008600; TNF_5; 1.
CC      ProDom; PD002012; TNF_subf; 1.
CC      SMART; SM00207; TNF; 1.
CC      PROSITE; PS00251; TNF 1; 1.
CC      PROSITE; PS00049; TNF 2; 1.
KW      Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT      CHAIN          1      272
FT      CHAIN          111
FT      CHAIN          272
FT      DOMAIN          1      23
FT      TRANSMEM          24      44
FT      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT      (POTENTIAL).
FT      DOMAIN          45      272
FT      SITE          110      111
FT      CLEAVAGE (BY SIMILARITY).
FT      DISULFID          190      229

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Query Match 12.4%; Score 184; DB 1; Length 272;
Best Local Similarity 25.4%; Pred. No. 5.1e-08;
Matches 69; Conservative 48; Mismatches 119; Indels 36; Gaps 9;

FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 272 AA; 30832 MW; 8CD0338A924E044B CRC64;

QY 16 CVLIIVFTVLLQSLCVAVTVYVFTNELKQMDQKYSKSGIACFLKEDDSYWDNDRESMNS 75
Db 26 CFLSVFMVY-QTIGTVLFLVLMKMDKNEEVLSDNYIIFIRKVKQCTGDDOKSTLL 83
QY 76 PCMQVQWQLRQLVRKMLTSETISTVQEKQONISPLVRERG-----QRVAAHIT 127
Db 84 DCEKVLKGFQDLQCKD--RTASEELPKFEMHGRGHEPHLKSNETSVAAEKKQPIATHLA 141
QY 128 GTRGRSNTLSSPNSKNEKALGRKINSW-ESSRSGHSFSLNHLRNGELVIHEKGFYIYS 186
Db 142 GV--KSNTTV-----RVLKMMTTSYAPTSSLSISYH--EGKLKVEKAGLYIYS 185
QY 187 QTYFRFOBEIKENTKNDKQMVQYIYKYTSYPDPILLKMSARNSCWSKDAEYGLYSIYOGG 246
Db 186 QVSF-----CTKAAASAPFTLYIYLYLPMEDRLIMKGLDTHST--TALCELOSIREGG 238
QY 247 IPELKENDRIFVSVTNEHLIDMDHEASFFQAF 278
Db 239 VPELRQGMVFVNVTSTAVNVNPGNTYFGMF 270

RESULT 11
TNF6_PIG
ID TNF6_PIG STANDARD; PRT; 282 AA.
AC Q9BEA8; Q95M04; Q95N10;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE ligand).
GN TNFSF6 OR FASL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactylia; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21322533; PubMed=11429161;
RA Muneta Y., Shimoi Y., Inumaru S., Mori Y.;
RT "Molecular cloning, characterization, and expression of porcine Fas
RT ligand (CD95 ligand).";
RL J. Interferon Cytokine Res. 21:305-312(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Guanxi bama miniature pig;
RA Zhu N., Young Y.;
RT "Molecular cloning and characterization of porcine Fas ligand cDNA.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Tsuyuki S., Kono M., Bloom E.T.;
RT "Cloning and potential utility of porcine Fas ligand: overexpression
RT in porcine cells protects them from attack by human cytolytic cells.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocytes;
RX MEDLINE=21653191; PubMed=11792426;
RA Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
RT "Porcine Fas-ligand gene: genomic sequence analysis and comparison
RT with human gene.";
RL Mol. Immunol. 38:581-586(2002).
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RX MEDLINE=99091541; PubMed=9872942;
RA Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
RA Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
RA Li L.-Y., Gentz R., Yu G.-L.;
RT "VEG1, a novel cytokine of the tumor necrosis factor family, is an
RT angiogenesis inhibitor that suppresses the growth of colon carcinomas
RT in vivo";
RL FASEB J. 13:181-189(1999).
CC -1- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
CC (in vitro).
CC -1- SUBUNIT: Homotrimer (Potential).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
CC Detected in placenta, lung, kidney, skeletal muscle, pancreas,
CC spleen, prostate, small intestine and colon.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC -----
DR EMBL; AF039390; AAD08783.1; -
DR HSP; P50591; IDOG.
DR Genew; HGNC:11931; TNFSF15.
DR MIM; 604052; -
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0005102; F: receptor binding; TAS.
DR GO; GO:000074; P: regulation of cell cycle; TAS.
DR InterPro; IPR006053; TNF_family.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNFECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; signal-anchor.
FT DOMAIN 1 12
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT TRANSMEM 13 25
FT
FT DOMAIN 26 174
FT EXTRACELLULAR (POTENTIAL).
FT DISULFID 85 125
FT POTENTIAL.
FT CARBOHYD 56 56
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 174 AA; 20131 MW; CCB83BA7EE673B98 CRC64;
Query Match 10.8%; Score 160; DB 1; Length 174;
Best Local Similarity 35.3%; Pred. No. 2.7e-08;
Matches 49; Conservative 24; Mismatches 48; Indels 18; Gaps 8;
Qy 154 WESSRSGHSLN-LHLRNGELVTHKGFVYVYQTVFRFQ-----EIKENTKDK--QM 206
Db 42 WE-HELGLAFKRMVNTNFKLLPESGDFYISQVTFRGMTSECSIRQAGRNKEDSI 100
Qy 207 VQYIKYKT-SYPDPILLMKSRNSCWSKDAFYG---LYSYQGQIFELKENDRIFVSVTN 262
Db 101 TWVITKVTDSYPEPTQLLMGKTSVC-----EVGSNWQPIYLGAMFSLQSGDKLMVNVSD 155
Qy 263 EHLIDMDHE-ASFGFGLV 280
Db 156 ISLDVYTKEDKTFGFAELL 174

RESULT 15
TN14 HUMAN
ID TN14 HUMAN STANDARD; PRT; 240 AA.
AC Q43557; O75476; Q8WVF8; Q96LD2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
DE mediator-ligand) (HVEM-L).
GN TNFSF14 OR LIGHT OR HVEM-L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98122340; PubMed=9462508;
RA Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
RA Ware C.F.;
RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
RT ligands for herpesvirus entry mediator";
RL Immunity 8:21-30(1998).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RP TISSUE=Liver;
RX MEDLINE=98438532; PubMed=9765287;
RA Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
RA Tan K.B., Dede K., Spanpanato J., Silverman C., Hensley P.,
RA DiPrinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
RA Truneh A., Young P.R.;
RT "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
RT HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell
RT growth";
RL J. Biol. Chem. 273:27548-27556(1998).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
RX MEDLINE=21528948; PubMed=11673523;
RA Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
RT "Genomic characterization of LIGHT reveals linkage to an immune
RT response locus on chromosome 19p13.3 and distinct isoforms generated
RT by alternate splicing or proteolysis";
RL J. Immunol. 167:5122-5128(2001).
RN [4]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalou D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinska M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Cytokine that binds to TNFSF3/LTBR. Binding to the
CC decoy receptor TNFSF6B modulates its effects. Activates NFkB,
CC stimulates the proliferation of T cells, and inhibits growth of
CC the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex

CC virus.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC (isoform 1); Cytoplasmic (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O43557-1; Sequence=displayed;
CC Name=2; Synonyms=LIGHT delta-TM;
CC IsoId=O43557-2; Sequence=VSP_006452;
CC TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
CC FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
CC TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
CC AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
CC NONHEMATOPOIETIC TUMOR LINES.
CC -!- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
CC -!- PTM: N-glycosylated.
CC -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC by proteolytic processing.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 178.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF036581; AAC39563.1; -
CC EMBL; AF064090; AAC25169.1; -
CC EMBL; AY028261; AAK26160.1; -
CC EMBL; BC018058; AAK18058.1; ALT_FRAME.
CC HSSP; P01375; 4TSV.
CC Genew; HGNC:11930; TNFSF14.
CC MIM; 604520; -
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0006917; P:induction of apoptosis; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR006053; TNF abc.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF-like.
CC Pfam; PF00229; TNF; 1
CC PRINTS; PR01234; TNFCROSIPTCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF 1; FALSE_NEG.
CC PROSITE; PS00049; TNF 2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
CC Alternative splicing.
CC CHAIN 1 240
CC CHAIN ?83 240 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC CHAIN MEMBER 14, MEMBRANE FORM.
CC CHAIN TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC DOMAIN 1 37 MEMBER 14, SOLUBLE FORM.
CC TRANSMEM 38 58 CYTOPLASMIC (POTENTIAL).
CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC DOMAIN 59 240 EXTRACELLULAR (POTENTIAL).
CC SITE 82 83 CLEAVAGE (POTENTIAL).
CC DISULFID 154 187 POTENTIAL.
CC CARBOHYD 102 102 N-LINKED (GLCNAC...).
CC VARSPLIC 38 73 Missing (in isoform 2).
CC CONFLICT 120 120 /FTIG=VSP_006452.
CC CONFLICT 214 214 L -> V (IN REF. 4).
CC CONFLICT 214 214 E -> K (IN REF. 2).
CC SEQUENCE 240 AA; 26351 MW; 49DOB67E1390B39 CRC64;

Query Match 10.8%; Score 159.5; DB 1; Length 240;
Best Local Similarity 23.8%; Pred. No. 4.6e-06;
Matches 53; Conservative 41; Mismatches 66; Indels 63; Gaps 9;

QY 79 QVKNQRLQRLVRKMLTSETISTVQKQON-ISPLVRERGPORVAHITGTRGNTLS 137
Db 60 QLHWRLGEMVTRLPDGPAGSWEQLIOERSHEVNP-----AAHLTGANSSITGSG 109
QY 138 SPNSKNEKALGRKINSWSSRSRSHSPLSNHLRNGELVIHEKGFYIYSQTVRFQEEIK 197
Db 110 GP-----LLWE-TOLGLAFLRGLSYHDGALVVTKAGYVYISK----- 146
QY 198 ENTKNQKQMVQY-----LYKYT-SYDPEILLMKSAKNSCWSKDAEYGLY 240
Db 147 -----VQLGGVCCPLGLASTITHGLYKTPRYPEELELLVSSQSPCGRATSSRW 197
QY 241 --SIYGGGIFELKENDRIFVSVTNEHLDM-DHEASFFGAFV 280
Db 198 WDSFSLGGVYVHLEAGEVVRVLDRLVRLDTRSYFGAFV 240

Search completed: March 23, 2004, 09:05:48
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:04:03 ; Search time 45 Seconds
(without alignments)
1970.236 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMEVQGGPSLGTCVLIY.....NEHLIDMDEASFFGAFVVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	963	65.2	287	11	Q8K3G0
2	809.5	54.8	304	13	Q7TIF2
3	334.5	22.6	317	13	Q7ZYX9
4	307.5	20.8	287	13	Q90WT9
5	305.5	20.7	214	13	Q9DDZ5
6	184.5	12.5	279	11	Q7TMV9
7	180	12.2	252	11	Q8K3Y8
8	178.5	12.1	280	6	Q861W5
9	175.5	11.9	169	11	Q9WV90
10	175	11.8	252	11	Q80Y20
11	173	11.7	252	11	Q8K3Y7
12	166	11.2	251	4	Q8NFE9
13	157	10.6	154	6	Q8MJ19
14	153.5	10.4	227	13	Q7T2Q3
15	144.5	9.8	216	11	O70332
16	141	9.5	231	13	Q8AW02

17	137.5	9.3	232	11	Q80XA4
18	135	9.1	156	11	Q91ZL4
19	135	9.1	215	6	Q9BEE8
20	135	9.1	217	11	Q9ERG6
21	130.5	8.8	222	13	Q7T1U4
22	130.5	8.8	225	13	Q9IB41
23	130.5	8.8	225	13	Q9IB42
24	128	8.7	230	13	Q8JG37
25	127	8.6	253	13	Q7T194
26	126.5	8.6	215	11	Q99ND1
27	124	8.4	216	6	Q9BEC4
28	123.5	8.4	216	6	Q9BEC9
29	122	8.3	205	4	Q8M4C3
30	121.5	8.2	246	13	Q9I976
31	121.5	8.2	246	13	Q9I970
32	120	8.1	237	13	Q8AWC9
33	119	8.1	202	11	Q80WE7
34	116.5	7.9	217	6	Q9BEG0
35	116.5	7.9	217	6	Q9BEF4
36	115.5	7.8	149	6	O97543
37	113.5	7.7	255	13	Q9I8I0
38	113.5	7.7	255	13	Q9DEP9
39	112.5	7.6	217	6	Q9BEG1
40	112.5	7.6	638	8	Q9Z2W6
41	110	7.4	93	6	Q9T1J2
42	109.5	7.4	149	6	O97538
43	109.5	7.4	149	6	Q9T7G8
44	109	7.4	288	13	Q8JHJ4
45	109	7.4	652	11	Q60421

ALIGNMENTS

RESULT 1

Q8K3G0 PRELIMINARY; PRT; 287 AA.

AC Q8K3G0;
 DT 01-OCT-2002 (TREMREL. 22, Created)
 DT 01-OCT-2002 (TREMREL. 22, Last sequence update)
 DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
 DE TNF-related apoptosis inducing ligand.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DA;
 RA Mueller A.M., Giegerich G.;
 RT "Rattus norvegicus TNF-related apoptosis inducing ligand (TRAIL).";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY115578; AAM49797.1; -;
 DR GO; GO:0016020; C-membrane; IEA.
 DR GO; GO:0005164; F-tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0008955; P-immune response; IEA.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF like.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF subf. 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF 1; 1.
 DR PROSITE; PS0049; TNF 2; 1.
 SQ SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;

Query Match 65.2%; Score 963; DB 11; Length 287;

Best Local Similarity 67.7%; Pred. No. 2.7e-72;

Matches 189; Conservative 29; Mismatches 51; Indels 10; Gaps 3;

QY 9 GPSLQG---TCVLIVFTVLQSLCAVTVYVYFTNELKQMODKYSKSGIACFLKDDSY 64

DB 9 GFSFSQHFMTVICIVLLQVLQAVTVMYFNNEVQLQDNYSKIGLACFSKDGDF 68


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QY 65 WDNDESMNSPCQVQWQLRQLVRLKMLRTSBETISTVOEKQONTSPILVRERGQVAA 124
DB 69 WDSDEGILNRPCLQVKRQYQLIEEVTLTFTKTIPTVEKQLSTPPLPRGRRPQVAA 128
QY 125 HINGTRGRNTLSSPNSKNEKALGRKINSWESSRSHSFLSNLHLRNGELVTHEKGFYIT 184
DB 129 HITGTRFRSMALIPISKOKTLGQKIEWESSRRGHSLHNVHLRNGELVTHEGLYI 188
QY 185 YSQTYFRFQEB--BIKENTKND-----KQVQYIYKYTSYPPILLMKSARNSCWSKDAEY 238
DB 189 YSQTYFRFKEAKASKTVSKDGGRIKQVQYIYKYTSYPPILLMKSARNSCWSREAYG 248
QY 239 LYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGA 277
DB 249 LYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGA 287

RESULT 2
Q7T1F2 PRELIMINARY; PRT; 304 AA.
AC Q7T1F2;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Tumor necrosis factor related apoptosis inducing ligand.
GN TRAIL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Sayed A.A., Horiuchi H.H., Furusawa S., Matsuda H.;
RT "Identification and Characterization of Chicken TNF-superfamily
RT Ligand 8 (CD30 Ligand) and 10 (Tumor Necrosis Factor Related Apoptosis
RT Inducing Ligand TRAIL).";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB114678; BAC79267.1; -.
SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 54.8%; Score 809.5; DB 13; Length 304;
Best Local Similarity 55.4%; Pred. No. 1.9e-59;
Matches 160; Conservative 45; Mismatches 65; Indels 19; Gaps 6;

QY 8 GGSLSGQTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYKSGIACFLKEDDSYWD 67
DB 5 GGSPPAHTCGAVLVAALLQSVCAVAVTYVFTNELKQMDYSGTGACLTGELGLD 64
QY 68 N-----DESMNSPCQVQWQLRQLVRLKMLRTSBETISTVQ-EKQONTSPILVRERGQ- 120
DB 65 NLDVBSKDRVADPCQVQWHLGKLIKQWMSRILOENMSAINDRGTQALS--RDEFPQ 122
QY 121 ---RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSHSFLSNLHLRNGELV 177
DB 123 PTLRIAAHLTGSKRASA-SPHNYLSYRGIGKIHWSERRSHSFLYNVELNGLVLP 181
QY 178 EKGFYIYQTYFRFQEB-----IKENTKNDKQVQYIYKYTSYPPILLMKSARNSCW 231
DB 182 QTGFYIYQTYFRFQEBDEDESGLLERIKNPQLVQYIYKLTNPDPILLMKSARTSCW 241
QY 232 SKDAEGLYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAPLV 280
DB 242 SKKAEGLYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAFMI 290

RESULT 3
Q7ZYX9 PRELIMINARY; PRT; 317 AA.
AC Q7ZYX9
DT 01-JUN-2003 (TremBLrel. 24, Created)
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DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Similar to tumor necrosis factor (Ligand) superfamily, member 10.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044336; AAH44336.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;

Query Match 22.6%; Score 334.5; DB 13; Length 317;
Best Local Similarity 29.2%; Pred. No. 8.7e-20;
Matches 83; Conservative 55; Mismatches 113; Indels 33; Gaps 8;

QY 18 LVIIVTLLQSLCAVAVTYVFTNELKQMDKYKSGIACF-----LKEDDSYWDND-EE 71
DB 40 MVIVVVLQSLASTTGLFVYLNLSQVSKQVTELRCLGLNLVGLKQDQI--PEDLAQ 97
QY 72 SMNSPCQVQWQLRQLVRLK-----ILRTSEETISTVQEKQONTSPILVRERGQ 120
DB 98 LRGEPCMKLAEGIKAVISKVTDLSIKQTLHAARTHTSYNTGSKFMTV-----MQ 150
QY 121 RVAAHITGRGRNT-----LSSPNSKNEKALGRKINSWESSRSHSFLSNLHLRNGELV 175
DB 151 RFSAHLTLSSASDNRPSQDMHQPFDLHSCRFVHTW-ANKSFGAHLNMTLTNGRLR 209
QY 176 IHEKGFYIYQTYFRF-QEELKENTKNDKQVQYIYKYTSYPPILLMKSARNSCWSKD 234
DB 210 VPQDERYLYSQVYFRYPSDSDQSSVSHQLVQCIYKTSYLNPIQLLKGVTKWAPD 269
QY 235 AEYGLYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAF 278
DB 270 AEYALHSYVQGGIFELRAGDEVFVSVGPTVMVYGEDSSSYFGAF 313

RESULT 4
Q90WT9 PRELIMINARY; PRT; 287 AA.
AC Q90WT9;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE TNF-related apoptosis inducing ligand.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
RT ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057941; AAL23702.1; -.
DR HSSP; O35235; 11QA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
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Db 202 NQNLHVKVNRNKKYEDLVIMEKRLNYCTT--GQIWAHSSHLGAVFNLTSAHLYVNI 259
QY 261 TNEHLIDMDHEAGFFGAF 278
Db 260 SQLSLINFESKTFPGFLY 277

RESULT 7
Q8K3Y8 ID Q8K3Y8 PRELIMINARY; PRT; 252 AA.
AC Q8K3Y8
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TNF superfamily ligand TLIA.
GN TNFSF15.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RX MEDLINE=21909416; PubMed=11911831;
RA Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA Carrell J.W., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT "TLIA is a TNF-like ligand for DR3 and TR6/DCR3 and functions as a T
RT cell costimulator.";
RT Immunity 16:479-492(2002).
DR ENBL; AF520786; AA077367.1; -.
DR MGD; MG1:2180140; Tnfslf15.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 252 AA; 27723 MW; BB901C9350119E0F CRC64;

Query Match 12.2%; Score 180; DB 11; Length 252;
Best Local Similarity 32.4%; Pred. No. 5.1e-07;
Matches 69; Conservative 26; Mismatches 80; Indels 38; Gaps 12;

QY 83 QLRVQRKMLRTSEETISTVQEKQKQNSPLVLRGPGQVAHITGTRGNTLSSPNSK 142
Db 63 QLRVPGKCDMLRAITTEERSE--PSPQVYSP---PRGKPR--AHLT-----IKKQTPAPHLK 112
QY 143 NE-KALGRKINSWESSRSGHSLN-LHLRNGELVIEHKGFYIYSQTYRFQEEI----- 196
Db 113 NQLSAL-----HWEDH-LGWAFTKNGKYNKSLVIESGDYFIYSQITRGTTSCVDI 166
QY 197 ---KENTKNDKQMVQIYKYTSYDPDILLMKASRNSC-----WSKDAEYGLYSIQGIF 248
Db 167 SRGRPNKPSITVITKVAADSYEPARLLTGSVCEISNNW-----FQSIYLGAMP 219
QY 249 ELKENDRIFVSTNEHLIDMDHE--ASFGAPLV 280
Db 220 SLEEGRLMNVSDISLVDTYKEDTKTFPGAPLL 252

RESULT 8
Q861W5 ID Q861W5 PRELIMINARY; PRT; 280 AA.
AC Q861W5;

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DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fas ligand.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99053606; PubMed=9839871;
RA Mizuno T., Endo Y., Momoi Y., Goto Y., Nishimura Y., Tsubota K.,
RA Mikami T., Ohno K., Watari Y., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning of feline Fas antigen and Fas ligand cDNAs.";
RL Vet. Immunol. Immunopathol. 65:161-172(1998).
DR ENBL; AB003280; BAC76426.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 280 AA; 31361 MW; 6AA7E2DE1F1A6B5C CRC64;

Query Match 12.1%; Score 178.5; DB 6; Length 280;
Best Local Similarity 21.2%; Pred. No. 7.7e-07;
Matches 58; Conservative 53; Mismatches 77; Indels 85; Gaps 11;

QY 16 CVLIVFTVLLQSLCVAV---TVVYPTNELKQMDKYSKSGIACFLKEDSDYNDPDES 72
Db 81 CLLVMEFFVLVALVGLGCMFQLHQLKELARESTSQHVASSLEKQIGQLNPSEK- 139
QY 73 MNSPCQVQKQRLVLRKMLRTSEETISTVQEKQKQNSPLVLRGPGQVAHITGTRG 132
Db 140 -----REL-----RKVAHLTG----- 150
QY 133 SNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHKGFYIYSQTYRPF 192
Db 151 -----KPNRSIPL-----EWEDT-YGIALVSGVKYKGGVLINDTGMVYVKVNF 198
QY 193 QBEIKENTKNDKQMVQIY-KYTSYDPDILLMK-SARNSC-----WSKDAEYGLYSIQG 245
Db 199 Q-----SCNNQPLNHKVYRNRSKYQDVLVMEGKMMNYCTTGQWWAR-----SSYL 245
QY 246 GFELKENDRIFVSTNEHLIDMDHEASFGAF 278
Db 246 AVNLTSAHLYVNVSELSVSESKTFPGFLY 278

RESULT 9
Q9WF90 ID Q9WF90 PRELIMINARY; PRT; 169 AA.
AC Q9WF90
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fas ligand (Fragment).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Marmota.

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OX NCBI_TaxID=9995;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20010026; PubMed=10540161;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RL chronic woodchuck viral hepatitis."
RL Clin. Exp. Immunol. 118:63-70(1999).
DR EMBL; AF152368; AAD38387.1; -.
DR HSSP; P50591; 1D4V.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON TER 1
FT NON TER 169
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 11.9%; Score 175.5; DB 11; Length 169;
Best Local Similarity 27.8%; Pred. No. 7.2e-07;
Matches 54; Conservative 39; Mismatches 58; Indels 43; Gaps 10;

QY 83 QLRVLRKMLRTSEETISTVQEKQNIPLVREGRQORVAAHITGRGRSNTLSSPNSK 142
Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
10 ELRESINQ---RNTPELS-----EQIGHSPSPDKALRAAHUT---GKPNSSSP--- 56

QY 143 NEKALGRKINSWESSRSGHSLNHLRNGELVTHEKGFYIYSQTYFRFQEEIKENTKN 202
Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
57 -----LEWEDT-YGISLSGVKYQKGLVNDTGLYFVYSKIYFRGQ-----SCN 100

QY 203 DKQWQVIY-KYTSYPPDILMK-SARNSC-----WSKDAEYGLYSTYQGGIFELKENDR 255
Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
101 NQPLSHKVVYKNSKYPQDLVMEGKNYCTTGQMWAR-----SSYLGAVFNF*SNDH 153

QY 256 IFVSVTNEHLIDMD 269
Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
154 LYVNSLSLINEF 167

RESULT 10
Q80YZO PRELIMINARY; PRT; 252 AA.
AC Q80YZO;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BN20K13.3 (tumor necrosis factor (ligand) superfamily, member 15).
DE TNFSF15.
GN TNFSF15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RA Sycamore N.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL691468; CAD83021.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

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DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 27725 MW; A63ABDDCC9E969E0F CRC64;

Query Match 11.8%; Score 175; DB 11; Length 252;
Best Local Similarity 31.9%; Pred. No. 1.3e-06;
Matches 68; Conservative 26; Mismatches 81; Indels 38; Gaps 12;

QY 83 QLRVLRKMLRTSEETISTVQEKQNIPLVREGRQORVAAHITGRGRSNTLSSPNSK 142
Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
63 QLRVPGKDCMLRAITEERSE-PSPOQVYSP---PRGKPR-AHUT-----IKKQTPAPHLK 112

QY 143 NE-KALGRKINSWESSRSGHSLN-LHLRNGELVTHEKGFYIYSQTYFRFQEEI---- 196
Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
113 NQLSAL-----HWEHD-LGWAFTKNGKYLKSLVIPESGDYFIYSQITFRGTSVCGDI 166

QY 197 ---KENTKNDKQWQVIYKYTSYPPDILMK-SARNSC-----WSKDAEYGLYSTYQGGIF 248
Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
167 SRGRPNKPDSTITWITKVAADSYPEPARLLTGSKSVCESINNW-----FQSLYLGAFTF 219

QY 249 ELKENDRIFVSVTNEHLIDMDHE-ASFFGAPLV 280
Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
220 SLEGRDLMVNVSDSLVDYTKEDTKTFGAFLL 252

RESULT 11
Q8K3Y7 PRELIMINARY; PRT; 252 AA.
AC Q8K3Y7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TNF superfamily ligand TL1A.
DE TNFSF15.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=21909416; PubMed=11911831;
RA Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT "TL1A is a TNF-like ligand for DR3 and TR6/DCR3 and functions as a T
RT cell costimulator."
RL Immunity 16:479-492(2002).
DR EMBL; AF520787; AA07368.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 28029 MW; 7789E6556D46F293 CRC64;

Query Match 11.7%; Score 173; DB 11; Length 252;

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Best Local Similarity 32.7%; Pred. No. 1.9e-06;
Matches 56; Conservative 23; Mismatches 62; Indels 30; Gaps 8;

QY 124 AHITGTRGNTLSSPNKNEKALGRKINSWSSRSGHSFLSN-LHLRNGELVIEHKGFY 182
Db 98 AHITIMR-----QTFVHLKNELA-----ALHWENN-LGMFTKRMNTNKFVLPESGDY 148

QY 183 YIYSQTYFRFQ-----BEIKENTKNDKQMVQYIYKYTSYPPILLMKSARNSC----- 230
Db 149 FIYSQITFRGTTSECGDISRVRPKPDSITVITTKVADSYPEPAHLLTGTKSVCEISSN 208

QY 231 WSKDAEGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHE-ASFGAFIV 280
Db 209 W-----FOPIYLGAMFSLSEGRMLMVNSDISLVDTYKEDTKTFFGAFLI 252

RESULT 12
Q8NF99 PRELIMINARY; PRT; 251 AA.
AC Q8NF99;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 25, Last annotation update)
DE TNF superfamily ligand TL1A.
GN TNFSF15
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21909416; PubMed=11911831;
RA Magone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakara J.P.,
RA Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT "TL1A is a TNF-like ligand for DR3 and TR6/DCR3 and functions as a T
RT cell costimulator.";
RL Immunity 16:479-492(2002).
DR EMBL; AF520785; AAM77366.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_abc;
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_subf.
DR InterPro; IPR003636; TNF_subf.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf. 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 251 AA; 28087 MW; 65ED70E367E3446D CRC64;

Query Match 11.2%; Score 166; DB 4; Length 251;
Best Local Similarity 33.2%; Pred. No. 7.4e-06;
Matches 62; Conservative 30; Mismatches 55; Indels 30; Gaps 12;

QY 107 QONISPLVRERGPRVAHITGTRGNTLSSPNKNE-KALGRKINSWSSRSGHSFLS 165
Db 82 QQVYAPLRADGDKPR--AHLTVVR-----QTPTQHFKNQFPAL-----HWE-HELGLAFTK 129

QY 166 N-LHLRNGELVIEHKGFIYSQTYFRFQ-----BEIKENTKNDK-QMVQYIYKYT-SYP 217
Db 130 NRMVYTKFLIPESGDYFIYSQTYFRGNTSECEIRQAGRPNKPDSTIVVTKVTDSP 189

QY 218 DPILLMKSARNCSWSDAEYXG---LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHE-AS 273
Db 190 EPTQLMGTKSVG-----EVGSNWFQPIYLGAMFSLQEGKLMVNSDISLVDTYKEDKT 244

QY 274 FFGAFIV 280
Db 245 FFGAFLL 251

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RESULT 13
Q8MJ19 PRELIMINARY; PRT; 154 AA.
AC Q8MJ19;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 25, Last annotation update)
DE Fas ligand CD178 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnould D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
RA Estaquier J.;
RT "Caspase-dependent and -independent cell death pathways characterize
RT pathogenic Simian Immunodeficiency Virus infection. Relationship with
RT disease evolution.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530076; AAM95636.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008084; Fas_ligand.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf. 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 17410 MW; 971A43779B029449 CRC64;

Query Match 10.6%; Score 157; DB 6; Length 154;
Best Local Similarity 27.4%; Pred. No. 2.2e-05;
Matches 46; Conservative 33; Mismatches 65; Indels 24; Gaps 6;

QY 95 TSEETISTVQEKQONISPLVRERGPRVAHITGTRGNTLSSPNKNEKALGRKINSW 154
Db 8 TSQKHTASLSLEKQIGHPSPPPEKKQKVAHLTG-----KPNRSMP-----EW 52

QY 155 ESSRSGHSFLSNLHLRNGELVIEHKGFIYSQTYFRFQEIKEKENTKNDKQMVQYIY-KY 213
Db 53 EUT-YGIVLLSGVYKKGGLVINEGLYFYYSKVFRGQ-----SCTNPLSHKVMRN 105

QY 214 TSYPDILLMKSARNCSWSDAEYGLYSIQGGIFELKENDRIFSVT 261
Db 106 SKYPQDLVNMVEGKWS-YCTTGQMWASHSYLGAVENTLTSADHLVNVVS 152

RESULT 14
Q7T2Q3 PRELIMINARY; PRT; 227 AA.
AC Q7T2Q3;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor-3 alpha.
GN TNF-3ALPHA.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RESULT 15
O070332 PRELIMINARY; PRT; 216 AA.
ID AC
O70332;
AC O70332;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor-alpha (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]__TaxID=10036;
RP SEQUENCE FROM N.A.
RX TISSUE=Spleen;
RC MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tyton V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998) .
DR EMBL; AF046215; AAC40100.1; -.
DR HSSP; P06804; 2TNF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0008955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR Prodom; PD002012; TNF subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:04:02 ; Search time 60 Seconds

(without alignments)
1323.264 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMEVGGPSLGTQTCVLIV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1478	100.0	281	2 AAW19777	AAW19777 Novel cyt
2	1478	100.0	281	2 AAW27134	AAW27134 Human apo
3	1478	100.0	281	2 AAW19787	AAW19787 Human apo
4	1478	100.0	281	2 AAW76829	AAW76829 Human TL2
5	1478	100.0	281	2 AAW56760	AAW56760 Human TRA
6	1478	100.0	281	2 AAW44354	AAW44354 Human AGP
7	1478	100.0	281	2 AAY01517	AAY01517 Protein a
8	1478	100.0	281	2 AAY27012	AAY27012 Human Apo
9	1478	100.0	281	3 AAY81956	AAY81956 Human Apo
10	1478	100.0	281	3 AAB24038	AAB24038 Human PRO
11	1478	100.0	281	3 AAB08545	AAB08545 Amino aci
12	1478	100.0	281	3 AAB28691	AAB28691 Human AGP
13	1478	100.0	281	4 AAB50977	AAB50977 Human PRO
14	1478	100.0	281	4 AAB67243	AAB67243 Human Apo
15	1478	100.0	281	4 AAE11031	AAE11031 Human TNF
16	1478	100.0	281	4 AAB48350	AAB48350 Human TL2
17	1478	100.0	281	5 ABB08133	ABB08133 Human TRA
18	1478	100.0	281	5 ABG31630	ABG31630 Human TRA
19	1478	100.0	281	5 AAU75062	AAU75062 Human TNF
20	1478	100.0	281	5 AAM51077	AAM51077 Human Apo
21	1478	100.0	281	5 ABP51954	ABP51954 Human Apo
22	1478	100.0	281	5 AAO19095	AAO19095 C neoform
23	1478	100.0	281	5 AAU79593	AAU79593 Human TNF
24	1478	100.0	281	6 ABG73861	ABG73861 Human Apo
25	1478	100.0	281	6 ABU10205	ABU10205 Human Apo

RESULT 1

AAW19777	ID	AAW19777	standard; protein; 281 AA.
XX	AC	AAW19777;	
XX	DT	22-SEP-1997	(first entry)
XX	DE	Novel cytokine Apo-2 ligand.	
XX	XX	Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.	
XX	OS	Homo sapiens.	
XX	Key	Location/Qualifiers	
FT	Peptide	1..281	
FT	Region	/note= "Claim 4"	
FT	Protein	1..14	
FT	Protein	/label= Cytoplasmic_region	
FT	Region	15..281	
FT	Region	/note= "Claim 3"	
FT	Protein	15..40	
FT	Protein	/label= Transmembrane_region	
FT	Region	41..281	
FT	Region	/note= "Claim 2"	
FT	Modified-site	41..281	
FT	Modified-site	109	
FT	Protein	/label= Glycosylation	
FT	Protein	/note= "putative N-linked glycosylation site"	
FT	Protein	114..281	
FT	Protein	/note= "Claim 1"	
XX	WO9725428-A1.		
XX	17-JUL-1997.		
XX	08-JAN-1997;	97WO-US000272.	
XX	09-JAN-1996;	96US-00584031.	
XX	(GETH) GENENTECH INC.		
XX	Ashkenazi AJ, Chuntharapai A, Kim KJ;		
XX	WPI; 1997-372867/34.		
XX	N-PSDB; AAT72796.		

ALIGNMENTS

ABU71443 Human neo
ABG72738 Human TNF
Aao29543 Human TRA
ABU08558 Human TNF
ABR42313 Human TRA
ABG71905 Human TRA
ABP60546 Human tum
Aae36258 Human TRA
Aao31151 Human TNF
ABO25125 Human TNF
ABD61471 Native hu
ADC35202 Human TNF
ADD14080 Human src
ADD19010 Human dis
ADE76953 Human pro
ADB61488 Human Apo
ABG72257 Human tum
ADB61478 Human Apo
ADB61477 Human Apo
ADB61479 Human Apo

26 1478 100.0 281 6 ABU71443
27 1478 100.0 281 6 ABG72738
28 1478 100.0 281 6 AAO29543
29 1478 100.0 281 6 ABU08558
30 1478 100.0 281 6 ABR42313
31 1478 100.0 281 6 ABG71905
32 1478 100.0 281 6 ABP60546
33 1478 100.0 281 6 AAE36258
34 1478 100.0 281 6 AAO31151
35 1478 100.0 281 6 ABO25125
36 1478 100.0 281 7 ABD61471
37 1478 100.0 281 7 ADC35202
38 1478 100.0 281 7 ADD14080
39 1478 100.0 281 7 ADD19010
40 1478 100.0 281 8 ADE76953
41 1475 99.8 281 7 ADB61488
42 1473 99.7 281 5 ABG72257
43 1473 99.7 281 7 ADB61478
44 1473 99.7 281 7 ADB61477
45 1473 99.7 281 7 ADB61479

PT Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
PT apoptosis for the treatment of breast and colon cancer.
XX
PS Claim 4; Fig 1a; 72pp; English.
XX
CC A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian
CC cell apoptosis. It is believed to be a member of the tumour necrosis
CC factor cytokine family. Its amino acid sequence was deduced from a cDNA
CC clone (AAW172796) isolated from a human placental cDNA library. Apo-2
CC ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
CC 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
CC transformed or transfected with a vector contg. Apo-2 ligand nucleic
CC acid. They can be used to induce apoptosis in mammals and to treat
CC pathological conditions such as cancer (esp. breast or colon cancer) or
CC to raise antibodies useful in diagnostic assays
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKOMQDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKOMQDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLNGELVIEHGK 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLNGELVIEHGK 180

QY 181 FYYISQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYYISQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 2
AAW27134
ID AAW27134 standard; protein; 281 AA.
XX
AC AAW27134;
XX
DT 02-APR-1998 (first entry)
XX
DE Human Apoptosis inducing molecule-I (AIM-I).
XX
KW Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
KW tumour necrosis factor ligand superfamily; AIM-I altered expression;
KW neoplasia inhibition; anti-inflammatory agent.
XX
OS Homo sapiens.
XX
XX WO9733899-A1.
XX
PD 18-SEP-1997.
XX
PF 14-MAR-1996; 96WO-US003773.
XX
PR 14-MAR-1996; 96WO-US003773.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM;
XX
DR WPI; 1997-470807/43.
DR N-PSDB; AAT85210.

XX
PT New isolated apoptosis inducing molecule-I - used to develop products for
PT the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
PT versus host disease or inflammation.
XX
PS Claim 2; Fig 1; 82pp; English.
XX
CC The present sequence represents a human Apoptosis inducing molecule-I
CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand
CC superfamily. The products can be used in the diagnosis and treatment of
CC disorders related to under-expression, over-expression or altered
CC expression of AIM-I. AIM-I or agonists can be used for treating
CC autoimmune disorders including systemic lupus erythematosus,
CC immunoproliferative disease lymphadenopathy (IPL),
CC angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit
CC neoplasia such as tumour cell growth, to treat restenosis, to regulate
CC haematopoiesis in endothelial cell development, to stimulate peripheral
CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or
CC osteoporosis, for preventing graft-host rejection, and as anti-
CC inflammatory agents, for treating endotoxic shock or to prevent
CC activation of HIV
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKOMQDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKOMQDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLNGELVIEHGK 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLNGELVIEHGK 180

QY 181 FYYISQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYYISQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 3
AAW19787
ID AAW19787 standard; protein; 281 AA.
XX
AC AAW19787;
XX
DT 24-SEP-1997 (first entry)
XX
DE Human apoptosis inducer cytokine TRAIL.
XX
KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
KW thrombotic microangioplasty; therapy.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Domain 1..18 /label= Cytoplasmic_domain 240
FT Domain 19..38 /label= Transmembrane_domain 240
FT Domain 39..281


```

FT FT /label= Extracellular domain
FT FT /note= "contains a receptor-binding region"
FT FT 89..90
FT FT Cleavage-site
FT FT /note= "potential KEX2 protease processing site"
FT FT 109..111
FT FT Modified-site
FT FT /note= "potential N-glycosylation site"
FT FT 149..150
FT FT Cleavage-site
FT FT /note= "potential KEX2 protease processing site"
XX XX WO9701633-A1.
XX XX 16-JAN-1997.
XX XX
XX XX 25-JUN-1996; 96WO-US010895.
XX XX
XX XX 29-JUN-1995; 95US-00496632.
XX XX 01-NOV-1995; 95US-00548368.
XX XX
XX XX (IMMV ) IMMUNEX CORP.
XX XX
XX XX Wilev SR, Goodwin RG;
XX XX
XX XX WPI; 1997-118715/11.
XX XX N-PSDB; AAT72847.
XX XX
XX XX TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
XX XX cells - useful for treating thrombotic microangiopathy, cancer and viral
XX XX infection and for use in assays.
XX XX
XX XX Claim 10; Page 43-44; 62pp; English.
XX XX
XX XX Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
XX XX (AAW19787) is a novel cytokine that induces apoptosis of certain target
XX XX cells, including cancer cells and virally infected cells. Its amino acid
XX XX sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in
XX XX vector pBC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
XX XX polypeptides) can be expressed in host cells and used in the treatment of
XX XX cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
XX XX to raise antibodies that may be useful for treating thrombotic
XX XX microangiopathies
XX XX
XX XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCTVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGTCTVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYDPDPILLMKSNCSWDAEYGLY 240
DB 181 FYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYDPDPILLMKSNCSWDAEYGLY 240
QY 241 SIYGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 4
AAW76829
ID AAW76829 standard; protein; 281 AA.
XX
XX
AC AAW76829;

XX XX 25-JAN-1999 (first entry)
XX XX Human TL2 protein.
XX XX
XX XX TR6; tumour necrosis factor related receptor; human; treatment; stroke;
XX XX inflammation; arthritis; septicemia; autoimmune disease; restenosis;
XX XX transplant rejection; infection; ischaemia; brain injury; bone disease;
XX XX acute respiratory disease syndrome; acquired autoimmune disease syndrome;
XX XX AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF;
XX XX TL2. tumour necrosis factor-related apoptosis-inducing ligand.
XX XX
XX XX Homo sapiens.
XX XX
XX XX EP870827-A2.
XX XX
XX XX 14-OCT-1998.
XX XX
XX XX 23-DEC-1997; 97EP-00310562.
XX XX
XX XX 14-MAR-1997; 97US-0041230P.
XX XX 09-MAY-1997; 97US-00853684.
XX XX 22-AUG-1997; 97US-00916625.
XX XX
XX XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX XX
XX XX Deen KC, Young PR;
XX XX
XX XX WPI; 1998-523156/45.
XX XX N-PSDB; AAV63096.
XX XX
XX XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding
XX XX polypeptide, antibody, agonist, antagonist, etc.
XX XX
XX XX Disclosure; Page 32-33; 34pp; English.
XX XX
XX XX This sequence represents the human tumour necrosis factor (TNF)-related
XX XX receptor, TR2 (also known as tumour necrosis factor-related apoptosis-
XX XX inducing ligand, TRAIL). This protein is used in a method resulting in
XX XX the isolation of the novel human TNF related receptor, TR6. TR6
XX XX polypeptides and polynucleotides can be used in the treatment of chronic
XX XX and acute inflammation, arthritis, septicemia, autoimmune diseases (e.g.
XX XX inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
XX XX host disease, infection, stroke, ischaemia, acute respiratory disease
XX XX syndrome, restenosis, brain injury, (acquired autoimmune disease
XX XX syndrome), AIDS, bone diseases, cancer (e.g. lympho-proliferative
XX XX disorders), atherosclerosis and Alzheimers disease
XX XX
XX XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCTVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGTCTVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYDPDPILLMKSNCSWDAEYGLY 240
DB 181 FYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYDPDPILLMKSNCSWDAEYGLY 240
QY 241 SIYGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

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RESULT 5
AAW56760
ID AAW56760 standard; protein; 281 AA.
XX
AC AAW56760;
XX
DT 05-AUG-1998 (first entry)
XX
DE Human TRAIL polypeptide.
XX
KW Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
KW cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..18
FT /note= "N-terminal cytoplasmic domain"
FT Region 19..38
FT /note= "transmembrane region"
FT Domain 39..281
FT /note= "extracellular domain"
XX
FN US5763223-A.
XX
PD 09-JUN-1998.
XX
PF 25-JUN-1996; 96US-00670354.
XX
PR 29-JUN-1995; 95US-00496632.
PR 01-NOV-1995; 95US-00548368.
XX
PA (IMMUNEX CORP.
XX
PI Goodwin RG, Wiley SR;
XX
WPI; 1998-347322/30.
DR N-PSDB; AAV29518.
XX
XX
PT DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful
PT for producing recombinant polypeptides for research and therapy of
PT leukaemia, lymphoma, melanoma and viral infections.
XX
PS Claim 1; Col 33-36; 28pp; English.
XX
XX
CC This represents a human tumour necrosis factor related apoptosis ligand
CC (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce
CC apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful
CC for producing the recombinant TRAIL polypeptides, which may be useful in
CC studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
CC (e.g. to isolate antigens for vaccine development). The polypeptides can
CC be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
CC treatment of blood or bone-marrow), or to treat viral infections
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLQGTCLVLIIVFTLLQSLCAVAVTYVFTNLKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLQGTCLVLIIVFTLLQSLCAVAVTYVFTNLKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIISPLVREGPQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNIISPLVREGPQ 120
QY 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFTLNHLRNGELVITHEKG 180
Db 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFTLNHLRNGELVITHEKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
RESULT 6
AAW44354
ID AAW44354 standard; protein; 281 AA.
XX
AC AAW44354;
XX
DT 28-MAY-1998 (first entry)
XX
DE Human AGP-1.
XX
KW Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
KW bone resorption; haematopoietic disease.
XX
OS Homo sapiens.
XX
FN WO9746686-A2.
XX
PD 11-DEC-1997.
XX
PF 06-JUN-1997; 97WO-US009895.
XX
PR 07-JUN-1996; 96US-00660562.
XX
PA (AMGE-) AMGEN INC.
XX
PI Johnson MJ, Simonet WS, Danilenko DM;
XX
WPI; 1998-042194/04.
DR N-PSDB; AAV15295.
XX
XX
PT Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -
PT useful for treating inflammation, bone resorption and haematopoietic
PT diseases.
XX
PS Claim 7; Page 36-37; 54pp; English.
XX
XX
CC The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
CC factor (TNF)-related protein, involved in inflammation, myelopoiesis and
CC bone resorption. It has the same nucleic acid and amino acid (aa)
CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or
CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,
CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat
CC haematopoietic diseases associated with reduction in the number of bone
CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
CC by disease, injury or exposure to myelosuppressive agents. Host cells,
CC transformed with expression vectors containing AGP-1 DNA, are used to
CC produce recombinant AGP-1
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLQGTCLVLIIVFTLLQSLCAVAVTYVFTNLKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLQGTCLVLIIVFTLLQSLCAVAVTYVFTNLKQMDKYSKSGIACFLKE 60

```

QY 61 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 QY 181 FYIYSOTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 DB 181 FYIYSOTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7
 AAY01517
 ID AAY01517 standard; peptide; 281 AA.
 AC AAY01517;
 DT 27-MAY-1999 (first entry)
 XX Protein associated with neurodegenerative and autoimmune diseases.
 DE Neurodegenerative disease; autoimmune disease; inflammatory disease;
 KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
 KW surface receptor; TRAIL protein.
 XX Homo sapiens.
 XX FR2766713-A1.
 XX 05-FEB-1999.
 XX 04-AUG-1997; 97FR-00010176.
 XX 04-AUG-1997; 97FR-00010176.
 XX (INMR) BIO MERIEUX.
 XX Rieger F, Belliveau JF, Perron H;
 XX WPI; 1999-156177/14.
 XX Use of polypeptide derived from TRAIL protein for diagnosis of
 PT degenerative disease - autoimmunity and inflammation, also useful in
 PT prevention or treatment, and similar use of corresponding ligand and
 PT nucleic acid.

Claim 2; Page 13; 21pp; French.
 The specification describes the use a polypeptide corresponding to at
 CC least the primary sequence of part of the present sequence to produce a
 CC diagnostic, prophylactic or therapeutic composition useful in cases of
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
 CC be used in treatment of neurodegenerative diseases, lupus erythematosus,
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
 CC nervous system cells, antigenic and specifically recognise the surface
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
 CC receptors, inhibiting formation of natural complex
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLQGTCLVIFVTLQSLCVAVTVYFTNELKQMDQKYSKGIACFLKE 60

DB 1 MAMMEVQGGPSLQGTCLVIFVTLQSLCVAVTVYFTNELKQMDQKYSKGIACFLKE 60
 QY 61 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 QY 181 FYIYSOTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 DB 181 FYIYSOTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8
 AAY27012
 ID AAY27012 standard; protein; 281 AA.
 AC AAY27012;
 DT 24-SEP-1999 (first entry)
 XX Human Apo-2 ligand (Apo-2L) polypeptide.
 DE Cytokine; Apo-2 ligand; apoptosis; cancer; autoimmune disorder;
 KW lupus; immune-mediated glomerular nephritis; human.
 XX Homo sapiens.
 XX OS
 XX WO9936535-A1.
 XX 22-JUL-1999.
 XX 15-JAN-1999; 99WO-US001039.
 XX 15-JAN-1998; 98US-00007886.
 XX 15-APR-1998; 98US-00060533.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;
 XX WPI; 1999-444397/37.
 XX N-PSDB; AAX86987.
 XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 PT in mammalian cancer cells.
 XX Claim 1; Fig 1A; 86pp; English.

This sequence represents a novel human cytokine, designated Apo-2 ligand
 (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGGTCLVIVIFVTLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMVEVGGPSLGGTCLVIVIFVTLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYWDNDDESNMSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DDSYWDNDDESNMSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 9
 AAY81956
 ID AAY81956 standard; protein; 281 AA.
 AC AAY81956;
 XX
 DT 10-JUL-2000 (first entry)
 DE
 DE Human Apo-2 ligand protein sequence.
 KW Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
 KW therapy; apoptosis; cancer.
 XX
 OS Homo sapiens.
 XX
 PN US6046048-A.
 XX
 XX 04-APR-2000.
 XX
 PF 08-JAN-1997; 97US-00780496.
 XX
 PR 09-JAN-1996; 96US-0009755P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Kim KJ, Ashkenazi AJ, Chuntharapai A;
 XX
 DR WPI; 2000-282690/24.
 DR N-PSDB; AAA07425.
 XX
 PT New isolated monoclonal antibodies having antigen specificity for Apo-2
 PT ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo
 PT -2 ligand serum, and for treating diseases associated with increased
 PT apoptosis.
 XX
 PS Claim 9; Fig 1a; 46pp; English.
 XX
 CC This sequence is the human Apo-2 ligand protein, which is recognised by
 CC monoclonal antibodies produced by the hybridoma cell lines of the
 CC invention. The hybridoma cell lines are deposited under the American Type
 CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
 CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
 CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
 CC tissues, or serum. The antibodies may also be employed as therapeutics.
 CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
 CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
 CC pathological conditions or diseases associated with increased apoptosis.
 CC They are also useful for the affinity purification of Apo-2 ligand from
 CC recombinant cell culture or natural sources. The Apo-2 ligand itself may
 CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells.
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGGTCLVIVIFVTLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMVEVGGPSLGGTCLVIVIFVTLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYWDNDDESNMSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DDSYWDNDDESNMSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 10
 AAB24038
 ID AAB24038 standard; protein; 281 AA.
 AC AAB24038;
 XX
 DT 25-JAN-2001 (first entry)
 DE
 DE Human PRO1096 protein sequence SEQ ID NO:51.
 XX
 KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 KW identification; tumorigenesis; anticancer; detection.
 XX
 OS Homo sapiens.
 XX
 PN WO2000053750-A1.
 XX
 XX 14-SEP-2000.
 XX
 PF 02-DEC-1999; 99WO-US028551.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028634.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
 XX
 DR WPI; 2000-594320/56.
 DR N-PSDB; AAC58120.
 XX
 PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit
 PT the growth of tumors in mammals, and to identify inhibitors of PRO
 PT polypeptide activity or expression.
 XX
 PS Claim 61; Fig 36; 226pp; English.
 XX
 CC The present invention describes an antibody that binds to a human protein
 CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
 CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
 CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
 CC activity and can be used to diagnose tumours in mammals, by detecting
 CC complex formation when the antibody is contacted with test cells.
 CC Increased expression of genes encoding (I) can also be detected to

CC diagnose tumours. Agents which inhibit the activity of (I), especially
 CC the antibodies, or an antisense oligonucleotide which hybridises to genes
 CC encoding (I), can be used to inhibit tumour growth, preferably by
 CC inducing cell death. Methods from the present invention can be used to
 CC identify compounds which inhibit the biological activity of (I). AAC58019
 CC to AAC58102 represent PCR primers and hybridisation probes used in
 CC examples from the present invention for human PRO sequences. AAC58103 to
 CC AAC58122 and AAC582401 to AAC582404 represent human PRO polynucleotide and
 CC protein sequences given in the exemplification of the present invention
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESNMSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120
 DB 61 DDSYWDPNDESNMSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 11
 AAB08545
 ID AAB08545 standard; protein; 281 AA.
 AC AAB08545;
 XX
 DT 20-DEC-2000 (first entry)
 XX
 DE Amino acid sequence of a human TRAIL polypeptide.
 XX
 KW Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;
 KW TNF related apoptosis-inducing ligand; tumour cell;
 KW TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;
 KW non-small cell lung carcinoma.
 XX
 OS Homo sapiens.
 XX
 PN W0200048619-A1.
 XX
 PD 24-AUG-2000.
 XX
 PF 15-FEB-2000; 2000WO-US003891.
 XX
 PR 16-FEB-1999; 99US-0120313P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Rosen GD;
 XX
 DR WPI; 2000-558253/51.
 DR N-PSDB; AAA64325.
 XX
 PT Killing of tumor cells, e.g. solid tumors or carcinoma, comprises
 PT administration of synergistic combination of diterpenoid diepoxide and
 PT tumor necrosis factor related apoptosis-inducing ligand.
 XX

PS Disclosure; Page 23-24; 29pp; English.
 XX
 CC The present sequence represents a human TRAIL (tumour necrosis factor
 CC (TNF) related apoptosis-inducing ligand) polypeptide. The specification
 CC describes a method for enhanced killing of tumour cells. The method
 CC comprises contacting a susceptible tumour cell with a synergistic mixture
 CC of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined
 CC dosage to kill at least 50 % of the cells. This mixture is synergistic,
 CC and so is active at lower doses and against otherwise resistant cell
 CC lines. The method is used for killing tumour cells, especially solid
 CC tumours or carcinomas (especially mammary carcinoma or non-small cell
 CC lung carcinoma)
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESNMSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120
 DB 61 DDSYWDPNDESNMSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGP 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 12
 AAB28691
 ID AAB28691 standard; protein; 281 AA.
 AC AAB28691;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Human AGP-1.
 XX
 KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
 KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
 KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
 KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
 KW transplant rejection; cardiovascular disease; arteriosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN W0200063253-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008004.
 XX
 PR 16-APR-1999; 99US-00293245.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Hsu H, Meng S;
 XX
 DR WPI; 2000-665240/64.
 DR N-PSDB; AAC67831.
 XX

PT Fusion protein of AGP-1 protein and an Fc region, used to treat
PT proliferative disorders, immune disorders, and virally-induced disorders.
XX Claim 3; Fig 2; 93pp; English.
XX The present sequence is human AGP-1, a type II transmembrane protein.
CC Fusion proteins comprising an Fc immunoglobulin region fused to the N-
CC terminal portion of the AGP-1 protein have been produced. The fusion
CC proteins can be used to induce apoptosis in a tissue, and to treat
CC proliferative disorders, immune disorders, or virally-induced disorders.
CC The proliferative disorders include cancers, such as breast, prostate,
CC lung or colon cancer. The viral infections include hepatitis, and
CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion
CC proteins have increased biological activity compared to the soluble AGP-1
CC proteins used in prior art therapies
XX
XX Sequence 281 AA;
SQ

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 DDSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKTSYPPDILLMKSARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKTSYPPDILLMKSARNCSWCKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 13
AAB50977
ID AAB50977 standard; protein; 281 AA.
XX
XX AAB50977;
XX DT 21-MAR-2001 (first entry)
XX
XX Human PRO1096 protein.
DE Human; PRO; cytostatic; neutropic; neuroprotective; respiratory general;
KW antinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
XX
XX Homo sapiens.
XX
XX WO200073348-A2.
XX
XX 07-DEC-2000.
XX
XX 30-MAY-2000; 2000WO-US014941.
XX
XX 02-JUN-1999; 99WO-US012252.
XX 22-JUN-1999; 99US-0140650P.
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.

29-OCT-1999; 99US-0162506P.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028634.
02-DEC-1999; 99WO-US028551.
03-DEC-1999; 99US-0170262P.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030999.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
02-MAR-2000; 2000WO-US005841.
03-MAR-2000; 2000US-0187202P.
10-MAR-2000; 2000WO-US006319.
15-MAR-2000; 2000WO-US006884.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
XX Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
XX WPI: 2001-016509/02.
XX N-PSDB; AAC91579.
XX
XX Twenty eight nucleic acids encoding PRO polypeptides which are useful for
XX treating various tumors, e.g. breast cancer, and other inflammatory,
XX angiogenic and immunological disorders.
XX
XX Claim 31; Fig 54; 188pp; English.
XX
XX The present sequence is one of twenty eight novel PRO polypeptides. The
XX PRO polypeptides and their agonists, including antibodies, peptides, and
XX small molecule agonists, may be used to treat various tumors, e.g.,
XX cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
XX cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
XX central nervous system cancer, melanoma or leukaemia. They are also
XX useful for treating other disorders such as neuronal, glial, astrocytal,
XX hypothalamic and other glandular, macrophagal, epithelial, stromal and
XX blastocoelec disorders, and inflammatory, angiogenic and immunological
XX disorders
XX
XX Sequence 281 AA;
SQ

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYKSGIACFLKE 60
Qy 61 DDSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
Db 61 DDSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKTSYPPDILLMKSARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKTSYPPDILLMKSARNCSWCKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14
AAB67243
ID AAB67243 standard; protein; 281 AA.

```

XX AC AAB67243;
XX 18-APR-2001 (first entry)
XX Human Apo2 ligand.
XX Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
XX Homo sapiens.
XX WO200100832-A1.
XX 04-JAN-2001.
XX 26-JUN-2000; 2000WO-US017579.
XX 28-JUN-1999; 99US-0141342P.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
XX O'Connell M, Pai R, Shahrokh Z, Simmons L;
XX WPI; 2001-123012/13.
XX Use of divalent metal ions for making Apo-2 ligand and in formulations
XX containing Apo-2 ligand for increasing yield and stability of ligand
XX trimers, useful for therapeutic applications.
XX Claim 6; Fig 1; 60pp; English.
XX The present invention relates to a formulation comprising Apo-2 ligand
XX and divalent metal ions. Apo-2 ligand and the formulation are useful for
XX treating cancers and viral infections. Addition of divalent metal ions
XX for making Apo-2 ligand and formulations containing Apo-2 ligand results
XX in increased yield and stability of Apo-2 ligand trimers
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 4; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDNDPNDDESMNSPCQVQWQLRQLVKRMILRTSEETISTVQEKQONISPLVRERGPO 120
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QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
QY 181 FYYIYSQTYFRFOEIKENTKNDKQVYIYKYTSYDPDILMKSGARNCSKDAEYGLY 240
DB 181 FYYIYSQTYFRFOEIKENTKNDKQVYIYKYTSYDPDILMKSGARNCSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 15
AAE11031
XX AAE11031 standard; protein; 281 AA.
XX AAE11031;
XX 18-DEC-2001 (first entry)
XX

```

```

DE XX Human TNF related apoptosis inducing ligand (TRAIL) protein.
KW XX Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
KW melanoma.
OS XX Homo sapiens.
PH XX Location/Qualifiers
FT 1..18
FT Domain /label= N_terminal_cytoplasmic_domain
FT 19..38
FT Region /label= Transmembrane_region
FT 39..281
FT Domain /label= Extracellular_domain
XX US6284236-B1.
XX 04-SEP-2001.
XX 26-MAY-1999; 99US-00320424.
XX 29-JUN-1995; 95US-00496632.
XX 01-NOV-1995; 95US-00548368.
XX 25-JUN-1996; 96US-00670354.
XX 26-MAR-1998; 98US-00048641.
XX 10-NOV-1998; 98US-00190046.
XX (IMMV ) IMMUNEX CORP.
XX Wilely SR, Goodwin RG;
XX WPI; 2001-595463/67.
XX N-PSDB; AAD18395.
XX New tumor necrosis factor related apoptosis inducing ligand polypeptides
XX for treating viral infections (e.g. bovine viral diarrhoea or human
XX immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
XX Claim 2; Col 45-48; 41pp; English.
XX The invention relates to a cytokine designated as tumour necrosis factor
XX (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
XX of certain target cells, including cancer cells and virally infected
XX cells. The TRAIL polypeptides are useful in killing cancer cells, in
XX treating viral infections (e.g. bovine viral diarrhoea or human
XX immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
XX melanoma), as a research reagent useful in studying apoptosis including
XX the regulation of programmed cell death. TRAIL DNA sequences may be
XX employed in developing a gene therapy approach to treating disorders
XX mediated by defective or insufficient amounts of TRAIL, in the production
XX of TRAIL polypeptides and as probes or primers in polymerase chain
XX reactions (PCR). The present sequence is human TRAIL protein
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 4; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDNDPNDDESMNSPCQVQWQLRQLVKRMILRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDNDPNDDESMNSPCQVQWQLRQLVKRMILRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180

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Db	181	FYIYQTYRFOBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY	240
QY	241	SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG	281
Db	241	SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG	281

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NEWS	8	OCT 28	BIOSIS file segment of TOXCENTER reloaded and enhanced
NEWS	9	NOV 24	MSDS-CCOHS file reloaded
NEWS	10	DEC 08	CABA reloaded with left truncation
NEWS	11	DEC 08	IMS file names changed
NEWS	12	DEC 09	Experimental property data collected by CAS now available in REGISTRY
NEWS	13	DEC 09	STN Entry Date available for display in REGISTRY and CA/CAPLUS
NEWS	14	DEC 17	DGENE: Two new display fields added
NEWS	15	DEC 18	BIOTECHNO no longer updated
NEWS	16	DEC 19	CROPU no longer updated; subscriber discount no longer available
NEWS	17	DEC 22	Additional INPI reactions and pre-1907 documents added to CAS databases
NEWS	18	DEC 22	IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields
NEWS	19	DEC 22	ABI-INFORM now available on STN
NEWS	20	JAN 27	Source of Registration (SR) information in REGISTRY updated and searchable
NEWS	21	JAN 27	A new search aid, the Company Name Thesaurus, available in CA/CAPLUS
NEWS	22	FEB 05	German (DE) application and patent publication number format changes
NEWS	23	MAR 03	MEDLINE and LMEDLINE reloaded
NEWS	24	MAR 03	MEDLINE file segment of TOXCENTER reloaded
NEWS	25	MAR 03	FRANCEPAT now available on STN
NEWS EXPRESS			MARCH 5 CURRENT WINDOWS VERSION IS V7.00A, CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP), AND CURRENT DISCOVER FILE IS DATED 3 MARCH 2004
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SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

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=> s human Fas ligand
L1 370 HUMAN FAS LIGAND

=> s l1 and mouse fas ligand
L2 7 L1 AND MOUSE FAS LIGAND

=> dup remove l2
PROCESSING COMPLETED FOR L2
L3 3 DUP REMOVE L2 (4 DUPLICATES REMOVED)

=> d l3 1-3 cbib abs

L3 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
1996:61419 Document No. 124:115474 Use of Fas ligand to suppress T lymphocyte-mediated immune responses. Bellgrau, Donald; Duke, Richard C. (University of Colorado, USA). PCT Int. Appl. WO 9532627 A1 19951207, 50 pp. DESIGNATED STATES: W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, ES, FI, GB, GE, HU, JP, KE, KG, KP, KR, KZ, LK, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, US, UZ, VN; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1995-US6742 19950526. PRIORITY: US 1994-250478 19940527; US 1995-378507 19950126.

AB Soluble mouse and **human Fas ligand** polypeptides and methods are useful for inhibiting T-lymphocyte-mediated immune responses, treating inflammation or preventing transplant rejection. The Fas ligand may be provided to the recipient mammal by a variety of means, including by direct administration of the Fas ligand or by providing the gene encoding the Fas ligand to a subject such that Fas ligand is synthesized by the subject. Also, antibody and monoclonal antibody against the mouse and **human Fas ligand** epitopes are claimed.

L3 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN

1996:402030 Document No. 125:84664 Novel mammalian Fas ligands and cDNAs encoding them and their use in the therapeutic regulation of apoptosis. Nagata, Shigekazu; Suda, Takashi; Takahashi, Tomohiro; Nakamura, Norio (Mochida Pharmaceutical Co., Ltd., Japan; Osaka Bioscience Institute). Eur. Pat. Appl. EP 675200 A1 19951004, 175 pp. DESIGNATED STATES: R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE. (English). CODEN: EPXXDW. APPLICATION: EP 1994-117761 19941110. PRIORITY: JP 1993-305975 19931110; JP 1993-342526 19931213; JP 1994-74344 19940318; JP 1994-180955 19940708; JP 1994-239363 19940907; JP 1994-278378 19941018.

AB Novel polypeptide ligands for the Fas antigen are identified, purified and characterized and cDNAs encoding them are cloned and expressed. These proteins may be manufactured for regulation of apoptosis by expression of the cloned cDNA for therapeutic use or in the preparation of antibodies. These proteins have a cytoplasmic domain, a transmembrane domain and extracellular domain and takes part in apoptosis. CDNAs for these ligands were cloned by panning of an expression library in COS-7 cells. Monoclonal antibodies to the ligand were prepared and shown to inhibit Fas ligand-induced apoptosis. Antisense oligonucleotides to the Fas gene were able to inhibit gene expression.

L3 ANSWER 3 OF 3 MEDLINE on STN DUPLICATE 1
95071350. PubMed ID: 7980502. Role of Fas ligand in apoptosis induced by hepatitis C virus infection. Mita E; Hayashi N; Iio S; Takehara T; Hijioka T; Kasahara A; Fusamoto H; Kamada T. (First Department of Medicine, Osaka University School of Medicine, Japan.) Biochemical and biophysical research communications, (1994 Oct 28) 204 (2) 468-74. Journal code: 0372516. ISSN: 0006-291X. Pub. country: United States. Language: English.

AB To investigate the role that Fas ligand plays in the apoptosis of hepatocytes induced by hepatitis C virus infection, we isolated a cDNA clone for **human Fas ligand** and examined the expression of Fas ligand in liver-infiltrating mononuclear cells obtained from patients with chronic hepatitis C. The amino acid sequence of **human Fas ligand** showed 76% and 77% identity with those of rat and **mouse Fas ligand**, respectively. When the expression of Fas ligand transcripts was tested by reverse transcription-polymerase chain reaction, the amplified signal was detected in liver-infiltrating mononuclear cells and peripheral blood mononuclear cells, whereas only a weak signal or none at all was detected in liver tissues. These findings suggest that the Fas ligand-Fas antigen system may play an important role in liver cell injury by hepatitis C virus infection.

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L4 1444 RUBEN S?/AU

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L5 21 L4 AND "AIM"

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PROCESSING COMPLETED FOR L5

L6 14 DUP REMOVE L5 (7 DUPLICATES REMOVED)

=> d 16 1-14 cbib abs

L6 ANSWER 1 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN

2004:39584 Document No. 140:87695 A new member of the TNF ligand superfamily and its use in treating immune disorders. Ebner, Reinhard; Yu, Guo-Liang; **Ruben, Steven M.**; Zhai, Yifan; Ullrich, Stephen (Human Genome Sciences, Inc., USA). U.S. Pat. Appl. Publ. US 2004009147 A1 20040115, 189 pp., Cont.-in-part of U.S. 6,635,743. (English). CODEN: USXXCO. APPLICATION: US 2003-375680 20030228. PRIORITY: US 1996-PV13923 19960322;

US 1996-PV30157 19961031; US 1997-822953 19970321; US 1998-3886 19980107; US 1998-27287 19980220; US 1998-PV75409 19980220; US 1999-252656 19990219; US 1999-PV124041 19990311; US 1999-PV137457 19990604; US 1999-PV142657 19990706; US 1999-PV148326 19990811; US 1999-PV168380 19991202; US 2000-523323 20000310; US 2002-PV360234 20020301.

AB A new member of the human TNF-Ligand superfamily, Apoptosis Inducing Mol. II (**AIM II**) is identified by sequence homol. for use in the treatment of immune disorders. The protein is a ligand for the TNF receptor TR6 and so may be used for the therapeutic induction of apoptosis or as a target for new drugs for the therapeutic inhibition of apoptosis. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft vs. host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 2 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 1

2003:537115 Document No.: PREV200300537649. Apoptosis inducing molecule II and methods of use. Ebner, Reinhard [Inventor, Reprint Author]; Yu, Guo-Liang [Inventor]; Ruben, Steven M. [Inventor]; Ullrich, Stephen [Inventor]; Zhai, Yifan [Inventor]. Guilford, CT, USA. ASSIGNEE: Human Genome Sciences, Inc.. Patent Info.: US 6635743 October 21, 2003. Official Gazette of the United States Patent and Trademark Office Patents, (Oct 21 2003) Vol. 1275, No. 3. <http://www.uspto.gov/web/menu/patdata.html>. e-file.

ISSN: 0098-1133 (ISSN print). Language: English.

AB The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid molecules are provided encoding a human Apoptosis Inducing Molecule II (**AIM II**). **AIM II** polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft versus host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 3 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN 2003:70974 Document No.: PREV200300070974. Apoptosis Inducing Molecule II and methods of use. Ebner, Reinhard [Inventor, Reprint Author]; Yu, Guo-Liang [Inventor]; Ruben, Steven M. [Inventor]; Zhang, Jun [Inventor]; Ullrich, Stephen [Inventor]; Zhai, Yifan [Inventor]. Rockville, MD, USA. ASSIGNEE: Human Genome Sciences, Inc.. Patent Info.: US 6495520 December 17, 2002. Official Gazette of the United States Patent and Trademark Office Patents, (Dec 17 2002) Vol. 1265, No. 3. <http://www.uspto.gov/web/menu/patdata.html>. e-file.

ISSN: 0098-1133 (ISSN print). Language: English.

AB The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid molecules are provided encoding a human Apoptosis Inducing Molecule II (**AIM II**). **AIM II** polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft versus host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 4 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

2003:42575 Document No.: PREV200300042575. Apoptosis inducing molecule II. Ebner, Reinhard [Inventor, Reprint Author]; Yu, Guo-Liang [Inventor]; **Ruben, Steven M.** [Inventor]. ASSIGNEE: Human Genome Sciences, Inc.. Patent Info.: US 6479254 November 12, 2002. Official Gazette of the United States Patent and Trademark Office Patents, (Nov 12 2002) Vol. 1264, No. 2. <http://www.uspto.gov/web/menu/patdata.html>. e-file. ISSN: 0098-1133 (ISSN print). Language: English.

AB The present invention relates to a novel member of the TNF-Ligand superfamily, Apoptosis Inducing Molecule II (**AIM II**). In particular, isolated nucleic acid molecules are provided encoding the human **AIM II** protein. **AIM II** polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease, graft versus host disease, and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 5 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN

2002:488138 Document No. 137:57591 Apoptosis inducing Molecule II and methods of use. Ebner, Reinhard; Yu, Guo-liang; **Ruben, Steven M.**; Zhang, Jun; Ullrich, Stephen; Zhai, Yifan (Human Genome Sciences, Inc., USA). U.S. Pat. Appl. Publ. US 2002081647 A1 20020627, 96 pp., Cont.-in-part of U.S. Ser. No. 27,287. (English). CODEN: USXXCO. APPLICATION: US 1999-252656 19990219. PRIORITY: US 1996-PV13923 19960322; US 1996-PV30157 19961031; US 1997-822953 19970321; US 1998-3886 19980107; US 1998-27287 19980220; US 1998-PV75409 19980220.

AB The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid mols. are provided encoding a human Apoptosis Inducing Mol. II (**AIM II**). **AIM II** polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft vs. host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 6 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN

2002:409195 Document No. 137:1567 Human apoptosis inducing molecule II and its cDNA and use thereof in drug screening and therapy. Ebner, Reinhard; Yu, Guo-liang; **Ruben, Steven M.**; Ullrich, Stephen (Human Genome Sciences, Inc., USA). U.S. Pat. Appl. Publ. US 2002064869 A1 20020530, 79 pp., Cont.-in-part of U.S. Ser. No. 822,953, abandoned. (English). CODEN: USXXCO. APPLICATION: US 1998-27287 19980220. PRIORITY: US 1996-PV13923 19960322; US 1996-PV30157 19961031; US 1997-822953 19970321.

AB The present invention relates to a novel member of the TNF-Ligand superfamily, Apoptosis Inducing Mol. II (**AIM II**). In particular, isolated nucleic acid mols. are provided encoding the human **AIM II** protein. **AIM II** polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The effect of **AIM II** on the cell growth are tested in breast cancer cell line or xenograft human breast carcinoma cell MDA in nude mice. Soluble **AIM II** can mediate cytotoxicity in HT-29 cell and stimulate secretion of IFN γ in human PBL cells. Cell surface expression of β -lymphokine receptor fusion protein LT β R-Fc or TR2-Fc fusion protein can block soluble **AIM II**-mediated cytotoxicity in HT-29 cells and **AIM II** can bind to LT β R specifically. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease, graft vs. host disease, and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 7 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
2000:645884 Document No. 133:242574 Apoptosis-inducing molecule II and for antitumor, antiarthritic, antiautoimmune, and other therapeutic use. Ebner, Reinhard; Yu, Guo-liang; **Ruben, Steven M.**; Zhai, Yifan; Ullrich, Stephen (Human Genome Sciences, Inc., USA). PCT Int. Appl. WO 2000053223 A1 20000914, 388 pp. DESIGNATED STATES: W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US6332 20000310. PRIORITY: US 1999-PV124041 19990311; US 1999-PV137457 19990604; US 1999-PV142657 19990706; US 1999-PV148326 19990811; US 1999-PV168380 19991202.

AB The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid mols. are provided encoding a human Apoptosis Inducing Mol. II (**AIM II**). **AIM II** polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft vs. host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 8 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
2000:628154 Document No. 133:236828 Tumor necrosis factor receptors 6 α and 6 β . Gentz, Reiner L.; Ni, Jian; Ebner, Reinhard; Yu, Guo-liang; **Ruben, Steven M.**; Feng, Ping (Human Genome Sciences, Inc., USA). PCT Int. Appl. WO 2000052028 A1 20000908, 332 pp. DESIGNATED STATES: W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US5686 20000303. PRIORITY: US 1999-PV121774 19990304; US 1999-PV124092 19990312; US 1999-PV131279 19990427; US 1999-PV131964 19990430; US 1999-PV146371 19990802; US 1999-PV168235 19991201.

AB The present invention relates to novel Tumor Necrosis Factor Receptor proteins. In particular, isolated nucleic acid mols. are provided encoding the human TNFR-6 α and -6 β proteins. TNFR-6 α and -6 β polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of TNFR-6 α and -6 β activity. Also provided are diagnostic methods for detecting immune system-related disorders and therapeutic methods for treating immune system-related disorders.

L6 ANSWER 9 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
1999:549380 Document No. 131:180813 Apoptosis-inducing molecule II, its encoding cDNA sequence, and therapeutic and clinical uses. Ebner, Reinhard; Yu, Guo-Liang; **Ruben, Steven M.**; Zhang, Jun; Ullrich, Stephen; Zhai, Yifan (Human Genome Sciences, Inc., USA). PCT Int. Appl. WO 9942584 A1 19990826, 224 pp. DESIGNATED STATES: W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE,

SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1999-US3703 19990219. PRIORITY: US 1998-PV75409 19980220; US 1998-27287 19980220.

AB The present invention relates to a member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid mols. are provided encoding a human Apoptosis-Inducing Mol. II (**AIM II**). The nucleic acid was discovered in a cDNA library derived from human macrophage ox LDL, and shown to contain an open reading frame encoding a protein of 240 amino acid residues. **AIM II** polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. **AIM II** is highly expressed in activated lymphocytes but not in cancer cells. The protein has potent antitumor activity in vivo and in vitro and both lymphotoxin β receptor and TR2 are required for **AIM II**-induced growth inhibition of cancer cells. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft vs. host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 10 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
1999:451368 Document No. 131:86868 Cloning and cDNA sequence encoding human apoptosis-inducing molecule II. Ebner, Reinhard; Ruben, Steven M. ; Yu, Guo-liang; Ullrich, Stephen (Human Genome Sciences, Inc., USA). PCT Int. Appl. WO 9935262 A2 19990715, 165 pp. DESIGNATED STATES: W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1999-US242 19990107. PRIORITY: US 1998-3886 19980107; US 1998-27287 19980220.

AB The present invention relates to a member of the tumor necrosis factor ligand superfamily, apoptosis-inducing mol. II (**AIM II**). In particular, isolated nucleic acid mols. are provided encoding the human **AIM II** protein. **AIM II** polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. **AIM II** is highly expressed in activated lymphocytes but not in cancer cells, and demonstrates enhanced apoptosis and potent in vivo anti-tumor activities. Both lymphotoxin β receptor and TR2 are required for **AIM II**-induced growth inhibition of cancer cells. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease, graft vs. host disease, and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 11 OF 14 MEDLINE on STN DUPLICATE 2
1999123371. PubMed ID: 9924296. Vertical cup/disc ratio in relation to optic disc size: its value in the assessment of the glaucoma suspect. Garway-Heath D F; Ruben S T; Viswanathan A; Hitchings R A. (Glaucoma Unit, Moorfields Eye Hospital, London.) British journal of ophthalmology, (1998 Oct) 82 (10) 1118-24. Journal code: 0421041. ISSN: 0007-1161. Pub. country: ENGLAND: United Kingdom. Language: English.

AB **AIMS:** The vertical cup/disc ratio (CDR) has long been used in the assessment of the glaucoma suspect, though the wide range of CDR values in the normal population limits its use. Cup size is related physiologically to disc size and pathologically to glaucomatous damage. Disc size can be measured at the slit lamp as the vertical disc diameter

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(DD). The ability of the CDR, in relation to DD, to identify glaucomatous optic discs was investigated. METHODS: 88 normal, 53 early glaucoma, and 59 ocular hypertensive subjects underwent stereoscopic optic disc photography and clinical biometry. Photographs were analysed in a masked fashion by computer assisted planimetry. The relation between vertical cup diameter and DD was explored by linear regression, and expressed in terms of CDR. The upper limit of normal was defined by the 95% prediction intervals of this regression (method 1) and by the upper 97.5 percentile for CDR (method 2). The sensitivity and specificity of CDR to identify an optic disc as glaucomatous was tested with these disc size dependent and disc size independent cut offs in small, medium, and large discs. RESULTS: The CDR was related to DD by the equation $CDR = (-1.31 + (1.194 \times DD))/DD$. The sensitivity in small, medium, and large discs was 80%, 60%, and 38% respectively for method 1 and 33%, 67%, and 63% respectively for method 2. Specificity was 98.9% (method 1) and 97.7% (method 2). CONCLUSIONS: The CDR, relative to disc size, is useful clinically, especially to assist in identifying small glaucomatous discs.

L6 ANSWER 12 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
 1997:640681 Document No. 127:288196 Apoptosis-inducing molecule II. Ebner, Reinhard; **Ruben, Steven M.**; Yu, Guo-Liang (Human Genome Sciences, Inc., USA; Ebner, Reinhard; Ruben, Steven M.; Yu, Guo-Liang). PCT Int. Appl. WO 9734911 A1 19970925, 89 pp. DESIGNATED STATES: W: AM, AU, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IL, JP, KG, KP, KR, KZ, LT, LV, MD, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, UA, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1996-US16966 19961031. PRIORITY: US 1996-13923 19960322.

AB The present invention relates to a novel member of the TNF-Ligand superfamily, Apoptosis-Inducing Mol. II (**AIM II**). In particular, isolated nucleic acid mols. are provided encoding the human **AIM II** protein. **AIM II** polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease, graft vs. host disease, and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 13 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
 1997:623179 Document No. 127:315580 Apoptosis-inducing molecule I and its encoding cDNA from human tissues. **Ruben, Steven M.** (Human Genome Sciences, Inc., USA; Ruben, Steven M.). PCT Int. Appl. WO 9733899 A1 19970918, 83 pp. DESIGNATED STATES: W: AM, AU, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KG, KP, KR, KZ, LT, LV, MD, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, UA, US, UZ, VN; RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1996-US3773 19960314.

AB The invention relates to apoptosis-inducing mol. I (**AIM-I**) polypeptides, polynucleotides encoding the polypeptides, methods for producing the polypeptides, in particular by expressing the polynucleotides, and agonists and antagonists of the polypeptides. **AIM-I** cDNA was discovered in a cDNA library derived from cells of a human pancreatic tumor and shown to contain an open reading frame encoding 281 amino acid residues with 48.6% similarity and 22.9% identity to human Fas ligand. Northern blot anal. shows that **AIM-I** mRNA is abundant in human heart, bone marrow, CD4+ and CD19+ peripheral blood lymphocytes, and less so in lung and kidney tissue. Cloning of human **AIM-I** cDNA was demonstrated by expression in Escherichia coli using the bacterial expression vector pQE9, expression in a baculovirus expression system using the pA2 vector, expression in COS cells using the pCDNAI/Amp vector, and gene therapeutic expression. The invention further relates to methods for utilizing such polynucleotides, polypeptides,

agonists and antagonists for applications, which relate, in part, to research, diagnostic and clin. arts.

L6 ANSWER 14 OF 14 MEDLINE on STN DUPLICATE 3
95260771. PubMed ID: 7742276. Pattern electroretinogram and peripheral colour contrast thresholds in ocular hypertension and glaucoma: comparison and correlation of results. **Ruben S T**; Arden G B; O'Sullivan F; Hitchings R A. (Electrodiagnostic Department, Moorfields Eye Hospital, London.) British journal of ophthalmology, (1995 Apr) 79 (4) 326-31. Journal code: 0421041. ISSN: 0007-1161. Pub. country: ENGLAND: United Kingdom. Language: English.

AB **AIMS**--Both pattern electroretinogram and peripheral colour contrast thresholds have been shown to be abnormal in glaucoma and ocular hypertension. This study evaluates each of these tests as tools for the early diagnosis of glaucoma, compares and contrasts the results, and examines the relation between the two tests in a large cohort of ocular hypertensive patients. **METHODS**--Transient and steady state pattern electroretinograms and peripheral colour contrast thresholds were performed in 45 normal, 37 glaucomatous, and 206 ocular hypertensive eyes. The results were analysed using receiver operating characteristic curves, together with evaluation of sensitivity and specificity of the tests. The relation between the two tests was examined by direct statistical correlation of the results. **RESULTS**--All tests showed high sensitivity and specificity for discriminating between normal and glaucomatous eyes. However, there was a significant difference between the two tests for the number of ocular hypertensives considered as abnormal. Forty per cent of ocular hypertensives had abnormal pattern electroretinogram compared with 30% with abnormal peripheral colour vision. Peripheral colour contrast thresholds showed a significant correlation with both transient and steady state pattern electroretinogram. **CONCLUSION**--Both of these tests have been shown to be promising new tools for the early detection of glaucoma but the number of ocular hypertensive patients showing abnormal results is rather higher than expected considering the natural history of the condition. Sensitivity in ocular hypertension may be increased by using a combination of both tests. The significant correlation between these psychophysical and electrophysiological tests is discussed.

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---Logging off of STN---

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Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	57.28	57.49
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	-7.62	-7.62

STN INTERNATIONAL LOGOFF AT 14:08:52 ON 23 MAR 2004